

CC chemokine antagonists of the invention comprise an amino acid
 CC substantially equivalent to a wild-type bovine CXCL8 sequence, but having
 CC a truncation of the first 2 amino acid residues of bovine CXCL8, and
 CC having the following amino acid substitutions: Arg for Lys-11 and Pro for
 CC Gly-31 (present sequence); Arg for Lys-11, Pro for Gly-31, and Gly for
 CC Pro-32 (see ABB79967); or Arg for Lys-11, Ser for Thr-12, Phe for His-13
 CC and Pro for Gly-31 (see ABB79969). These ELR-CXC chemokine antagonists
 CC are capable of binding to CXCR1 or CXCR2 in mammalian
 CC inflammatory cells. The invention provides these novel ELR-CXC chemokine
 CC receptor antagonists, polynucleotides encoding them, vectors and host
 CC cells (bacteria, protozoa, yeast, fungi, algae, plant cells and animal
 CC cells) and viral hosts containing an expression vector, methods of
 CC production, and methods of using these for treating an ELR-CXC chemokine-
 CC mediated pathology in a bovid or a human, especially ischaemia-
 CC reperfusion injury, endotoxaemia-induced acute respiratory distress
 CC syndrome, immune complex glomerulonephritis, bacterial pneumonia, or
 CC mastitis, where the chemokine binds to CXCR1 or CXCR2 receptors (all
 CC claimed). Experimental results show that the present CXCL8(3-73)K11R/G31P
 CC protein competitively inhibits CXCL8 binding to neutrophils, does not
 CC display neutrophil agonist activity, blocks neutrophil chemotactic
 CC responses to both CXCR1 and CXCR2 ligands, is an effective *in vitro*
 CC antagonist of the neutrophil chemokines expressed in bacterial pneumonia
 CC or mastitis lesions, and is highly efficacious in blocking endotoxin-
 CC induced neutrophilic inflammation *in vivo*

CC Sequence 72 AA;

Query Match Best Local Similarity 100.0%; Score 391; DB 5; Length 72;
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TELRCOCIRHTSTPHFPFKIKELRVIESPPHCENSEIIVKLTNGNEVCINPKRKWKVKV 60
 DB 1 TELRCOCIRHTSTPHFPFKIKELRVIESPPHCENSEIIVKLTNGNEVCINPKRKWKVKV 60

QY 61 QVFVRAEKODP 72
 DB 61 QVFVRAEKODP 72

RESULT 2
 ID ABB79964 standard; protein; 72 AA.

XX ABB79964;
 AC ABB79964;
 XX ABB79964;
 DT 19-DEC-2002 (first entry)

XX Bovine CXCL8(3-73)G31P, ELR-CXC chemokine receptor antagonist.

XX ELR-CXC; chemokine; receptor; antagonist; CXCL8; cattle;
 KW antiinflammatory; vasotropic; antibacterial; nephrotropic; mutant;
 XX mutein.

XX Bos taurus.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 29 /note= "wild-type Gly substituted by Pro"

PN MO200270565-A2.

XX 12-SEP-2002.

XX 01-MAR-2002; 2002WO-CA000271.

XX 01-MAR-2001; 2001US-0273181P.

XX (USRA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.

XX Gordon JR, Li F;

DR WPI; 2002-723251/78.
 DR N-PSDB; ABQ81432.

XX New ELR-CXC chemokine antagonist, useful for treating a CXC chemokine-
 PT mediated pathology, e.g. ischaemia-reperfusion injury or endotoxaemia-
 PT induced acute respiratory distress syndrome.

XX Disclosure; Page 57; 64p; English.

XX The present sequence is the protein sequence of a mutated bovine bovine
 CC CXCL8 protein comprising amino acids 3-73 of the wild-type sequence with
 CC substitution of the native Gly-31 residue by Pro. Claimed ELR-CXC
 CC chemokine antagonists of the invention comprise an amino acid
 CC substantially equivalent to a wild-type bovine CXCL8 sequence, but having
 CC a truncation of the first 2 amino acid residues of bovine CXCL8, and
 CC having the following amino acid substitutions: Arg for Lys-11 and Pro for
 CC Gly-31 (see ABB79966); Arg for Lys-11, Ser for Thr-12, Phe for His-13 and Pro
 CC (see ABB79967); or Arg for Lys-11, Ser for Thr-12, Phe for His-13 and Pro
 CC for Gly-31 (see ABB79969). These ELR-CXC chemokine antagonists are
 CC capable of binding to CXCR1 or CXCR2 in mammalian
 CC inflammatory cells. The invention provides these novel ELR-CXC chemokine
 CC receptor antagonists, polynucleotides encoding them, vectors and host
 CC cells (bacteria, protozoa, yeast, fungi, algae, plant cells and animal
 CC cells) and viral hosts containing an expression vector, methods of
 CC production, and methods of using these for treating an ELR-CXC chemokine-
 CC mediated pathology in a bovid or a human, especially ischaemia-
 CC reperfusion injury, endotoxaemia-induced acute respiratory distress
 CC syndrome, immune complex glomerulonephritis, bacterial pneumonia, or
 CC mastitis, where the chemokine binds to CXCR1 or CXCR2 receptors (all
 CC claimed). The present CXCL8(3-73)G31P protein is a highly effective
 CC antagonist of CXCL8 binding to cells

CC Sequence 72 AA;

Query Match Best Local Similarity 99.2%; Score 388; DB 5; Length 72;
 Matches 71; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TELRCOCIRHTSTPHFPFKIKELRVIESPPHCENSEIIVKLTNGNEVCINPKRKWKVKV 60
 DB 1 TELRCOCIRHTSTPHFPFKIKELRVIESPPHCENSEIIVKLTNGNEVCINPKRKWKVKV 60

QY 61 QVFVRAEKODP 72
 DB 61 QVFVRAEKODP 72

RESULT 3

ID ABB79967 standard; protein; 72 AA.

XX ABB79967;
 AC ABB79967;
 XX ABB79967;
 DT 19-DEC-2002 (first entry)

XX CXCL8(3-73)K11R/G31P/P32G, ELR-CXC chemokine receptor antagonist.

XX ELR-CXC; chemokine; receptor; antagonist; CXCL8; cattle;
 KW antiinflammatory; vasotropic; antibacterial; nephrotropic; mutant;
 XX mutein.

XX Bos taurus.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 9 /note= "wild-type Lys substituted by Arg"

FT Misc-difference 29 /note= "wild-type Gly substituted by Pro"

FT Misc-difference 30 /note= "wild-type Pro substituted by Gly"

PN MO200270565-A2.

XX 12-SEP-2002.
 PD
 XX
 XX 01-MAR-2002; 2002MO-CA000271.
 PF
 XX
 PR 01-MAR-2001; 2001US-0273181P.
 XX
 XX (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
 PA
 XX
 PI Gordon JR, Li F;
 PD
 DR WPI: 2002-723251/78.
 DR N-PSDB; ABQ81435.
 XX
 XX
 PT New ELR-CXC chemokine antagonist, useful for treating a CXC chemokine-mediated pathology, e.g. ischemia-reperfusion injury or endotoxemia-induced acute respiratory distress syndrome.
 PT
 XX
 PS Disclosure; Page 62; 64pp; English.
 XX
 CC The present sequence is the protein sequence of a mutated bovine bovine CXCL8 protein comprising amino acids 3-73 of the wild-type sequence with CC substitution of the native Gly-31 amino acid residue by Pro, and CC substitution of the native Lys-11 residue by Arg. Claimed ELR-CXC CC chemokine antagonists of the invention comprise an amino acid CC substantially equivalent to a wild-type bovine CXCL8 sequence, but having CC a truncation of the first 2 amino acid residues of bovine CXCL8, and CC having the following amino acid substitutions: Arg for Lys-11 and Pro for CC Gly-31 (see ABB79966); Arg for Lys-11, Pro for Gly-31, and Gly for Pro-32 CC (present sequence); or Arg for Lys-11, Ser for Thr-12, Phe for His-13 and CC Pro for Gly-31 (see ABB79969). These ELR-CXC chemokine antagonists are CC capable of binding to CXC receptors (CXCR1 or CXCR2) in mammalian CC inflammatory cells. The invention provides these novel ELR-CXC chemokine CC receptor antagonists, polynucleotides encoding them, vectors and host CC cells (bacteria, protozoa, yeast, fungi, algae, plant cells and animal CC cells) and viral hosts containing an expression vector, methods of CC production, and methods of using these for treating an ELR-CXC chemokine-mediated pathology in a bovid or a human, especially ischemia-reperfusion injury, endotoxaemia-induced acute respiratory distress CC syndrome, immune complex-type glomerulonephritis, bacterial pneumonia, or CC mastitis, where the chemokine binds to CXCR1 or CXCR2 receptors (all CC claimed).
 XX
 SQ Sequence 72 AA;
 Query Match 97.7%; Score 382; DB 5; Length 72;
 Best Local Similarity 98.6%; Pred. No. 2,4e-36;
 Matches 71; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TELRCQCIKTHSTPFHFKFKELRVIESPHGENSEIIVKLTNGNEVCINLPKKEKVKQKV 60
 DB 1 TELRCQCIKTHSTPFHFKFKELRVIESPHGENSEIIVKLTNGNEVCINLPKKEKVKQKV 60
 QY 61 QVFPKRAEKODP 72
 DB 61 QVFPKRAEKODP 72
 RESULT 4
 ABB79965
 ID ABB79965 standard; protein: 72 AA.
 AC ABB79965;
 XX
 DT 19-DEC-2002 (first entry)
 XX
 DE Bovine CXCL8(3-73)K11R, ELR-CXC chemokine receptor antagonist.
 XX
 KW ELR-CXC; chemokine; receptor; antagonist; CXCL8; cattle;
 KM antiinflammatory; vasotropic; antibacterial; nephrotropic; mutant;
 XX muteln.
 XX
 OS Bos taurus.

OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH
 PT MISC-difference 9 /note= "wild-type Lys substituted by Arg"
 FT
 XX
 XX W0200270565-A2.
 PN
 XX
 XX 12-SEP-2002.
 PD
 DR 01-MAR-2002; 2002MO-CA000271.
 DR
 XX
 PR 01-MAR-2001; 2001US-0273181P.
 XX
 XX (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
 PA
 XX
 PI Gordon JR, Li F;
 PD
 DR WPI: 2002-723251/78.
 DR N-PSDB; ABQ81435.
 XX
 XX
 PT New ELR-CXC chemokine antagonist, useful for treating a CXC chemokine-mediated pathology, e.g. ischemia-reperfusion injury or endotoxemia-induced acute respiratory distress syndrome.
 PT
 XX
 PS Disclosure; Page 58; 64pp; English.
 XX
 CC The present sequence is the protein sequence of a mutated bovine bovine CXCL8 protein comprising amino acids 3-73 of the wild-type sequence with CC substitution of the native Lys-11 residue by Arg. Claimed ELR-CXC CC chemokine antagonists of the invention comprise an amino acid CC substantially equivalent to a wild-type bovine CXCL8 sequence, but having CC a truncation of the first 2 amino acid residues of bovine CXCL8, and CC having the following amino acid substitutions: Arg for Lys-11 and Pro for CC Gly-31 (see ABB79966); Arg for Lys-11, Pro for Gly-31, and Gly for Pro-32 CC (see ABB79969); or Arg for Lys-11, Ser for Thr-12, Phe for His-13 and CC Pro for Gly-31 (see ABB79969). These ELR-CXC chemokine antagonists are CC capable of binding to CXC receptors (CXCR1 or CXCR2) in mammalian CC inflammatory cells. The invention provides these novel ELR-CXC chemokine CC receptor antagonists, polynucleotides encoding them, vectors and host CC cells (bacteria, protozoa, yeast, fungi, algae, plant cells and animal CC cells) and viral hosts containing an expression vector, methods of CC production, and methods of using these for treating an ELR-CXC chemokine-mediated pathology in a bovid or a human, especially ischemia-reperfusion injury, endotoxaemia-induced acute respiratory distress CC syndrome, immune complex-type glomerulonephritis, bacterial pneumonia, or CC mastitis, where the chemokine binds to CXCR1 or CXCR2 receptors (all CC claimed).
 XX
 SQ Sequence 72 AA;
 Query Match 97.7%; Score 382; DB 5; Length 72;
 Best Local Similarity 98.6%; Pred. No. 2,4e-36;
 Matches 71; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TELRCQCIKTHSTPFHFKFKELRVIESPHGENSEIIVKLTNGNEVCINLPKKEKVKQKV 60
 DB 1 TELRCQCIKTHSTPFHFKFKELRVIESPHGENSEIIVKLTNGNEVCINLPKKEKVKQKV 60
 QY 61 QVFPKRAEKODP 72
 DB 61 QVFPKRAEKODP 72
 RESULT 5
 ABB79969
 ID ABB79969 standard; protein: 72 AA.
 AC ABB79969;
 XX
 DT 19-DEC-2002 (first entry)
 XX
 DE CXCL8(3-73)K11R/T12S/H13F/G31P, CXC chemokine receptor antagonist.

DB 4 ELRCOCITKHSKPHPKFIKELRVIESGPHCANTTEIIVKSDGRELCLDPKENVQVRVE 63

QY 62 VFVKRAE 68
DB 64 KFLKRAE 70

RESULT 9

AAW25706
ID AAW25706 standard; protein, 72 AA.

AAW25706;

17-OCT-1997 (first entry)

DE Mutant human IL-8, R47K,D52N.

KM Interleukin-8; IL-8; IL-8 receptor-mediated biological response; mutant;
KW IL-8 receptor; overlap PCR.

OS Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 47 /label= R47K

FT Misc-difference 52 /label= D52N

PN W09700601-A2.

XX 09-JAN-1997.

PF 18-JUN-1996; 96WO-US010537.

PR 20-JUN-1995; 95US-0002774P.

PR 18-OCT-1995; 95US-0005385P.

PR 05-APR-1996; 96US-00628455.

PA (CHIR) CHIRON CORP.

PI Wernette-Hammond ME, Shyamala V, Siani M, Blaney J;
PI Tekamp-Olson P;

DR WPI; 1997-087095/08.

PT New mutant interleukin-8 poly:peptide(s) - used for modulating
PT Interleukin-8 receptor-mediated biological responses.

PS Claim 1; Page 34; 40pp; English.

CC The sequences given in AAW25701-14 represent interleukin-8 (IL-8) mutants
CC which are capable of binding to IL-8 receptors. They can be used for
CC modulating an IL-8 receptor-mediated biological response. The mutations
CC were introduced into the human IL-8 coding sequence by overlap PCR

XX SQ Sequence 72 AA;

Query Match 74.7%; Score 292; DB 2; Length 72;
Best Local Similarity 77.6%; Pred. No. 5.9e-26;
Matches 52; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 2 ELRCOCIRHTSTPFHFKFIKELRVIESGPHCENSEIIVKLTNGNEVCINPKKRWQKVVQ 61
DB 4 ELRCOCIRHTSTPFHFKFIKELRVIESGPHCANTTEIIVKSDGRELCLDPKENVQVRVE 63

QY 62 VFVKRAE 68
DB 64 KFLKRAE 70

RESULT 10
AAR38081
ID AAR38081 standard; protein; 69 AA.

XX AAR38081;

AC 25-MAR-2003 (revised)
XX 13-OCT-1993 (first entry)

DE Modified human interleukin-8 analogue (4-72).

KM Analogues; modified; neutrophil activators; antagonists; human;
KW competitive antagonist; IL-8; inflammation; treatment; chemotaxis;
KW activity; stimulation; inflammatory response.

OS Synthetic.

PN W09311159-A1.

PD 10-JUN-1993.

PF 03-DEC-1992; 92WO-CA000528.

PR 04-DEC-1991; 91US-00801578.

PA (BIOM-) BIOMEDICAL RES CENT LTD.

PI Clark-Lewis I, Moser B;

DR WPI; 1993-196997/24.

PT New interleukin-8 analogues modified in specified region - used as
PT neutrophil activators or for blocking effect of IL-8 on neutrophil(s),
PT for treatment of inflammation.

PS Claim 9; Page 29; 47pp; English.

CC The sequence is that of an analogue of interleukin-8 (IL-8) comprising IL
CC -8 residues 4-72. It is able to bind neutrophils and act as a competitive
CC antagonist of IL-8, i.e. it can be used to treat inflammation, e.g. by
CC intravenous injection or oral admin. It can act as a neutrophil activator
CC and so can be used to stimulate an inflammatory response. (Updated on 25-
CC MAR-2003 to correct PN field.)

XX SQ Sequence 69 AA;

Query Match 74.2%; Score 290; DB 2; Length 69;
Best Local Similarity 77.6%; Pred. No. 9.5e-26;
Matches 52; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 2 ELRCOCIRHTSTPFHFKFIKELRVIESGPHCENSEIIVKLTNGNEVCINPKKRWQKVVQ 61
DB 1 ELRCOCIRHTSTPFHFKFIKELRVIESGPHCANTTEIIVKSDGRELCLDPKENVQVRVE 60

QY 62 VFVKRAE 68
DB 61 KFLKRAE 67

RESULT 11
AAR38080
ID AAR38080 standard; protein, 72 AA.

XX AAR38080;

AC 25-MAR-2003 (revised)
DT 13-OCT-1993 (first entry)

DE Human interleukin-8 monomer.

KM Analogues; modified; neutrophil activators; antagonists; IL-8.

OS Homo sapiens.

PN W09311159-A1.

PD 10-JUN-1993.
XX 03-DEC-1992; 92WO-CA000528.
PF 04-DEC-1991; 91US-00801578.
XX (BIOM-) BIOMEDICAL RES CENT LTD.
PA Clark-Lewis I, Moser B;
PI WPI; 1993-19697/24.
XX New interleukin-8 analogues modified in specified region - used as
PT neutrophil activators or for blocking effect of IL-8 on neutrophil(s),
XX for treatment of inflammation.
XX Disclosure; Page 8; 47pp; English.
XX The sequence is that of the 72-residue form of the interleukin (IL-8)
CC monomer. It may be modified to produce biologically active analogues of
CC IL-8 which are able to bind neutrophils and act as competitive
CC antagonists of IL-8, i.e. they can be used to treat inflammation.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 72 AA;
Query Match 74.2%; Score 290; DB 2; Length 72;
Best Local Similarity 77.6%; Pred. No. 1e-25;
Matches 52; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
QY 2 ELRCQCIRHTSTPHPKFIFKELRVIESPPHCENSEIIVKLTNGNEVCLNPKRKWQVQ 61
DB 4 ELRCQCIRHTSTPHPKFIFKELRVIESPPHCENSEIIVKLTNGNEVCLNPKRKWQVQ 63
QY 62 VFVKRAE 68
DB 64 KFLKRAE 70
RESULT 12
AAW25704
ID AAW25704 standard; protein; 72 AA.
XX AAW25704;
AC 17-OCT-1997 (first entry)
XX
DT Mutant human IL-8, E48K, D52N.
XX
DE Interleukin-8; IL-8; IL-8 receptor-mediated biological response; mutant;
KM IL-8 receptor; overlap PCR.
XX
KW Homo sapiens.
XX
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 48 /label= E48K
FT Misc-difference 52 /label= D52N
FT
XX
PN WO9700601-A2.
XX
PD 09-JAN-1997.
XX
PF 18-JUN-1996; 96WO-US010537.
XX
XX 20-JUN-1995; 95US-0002774P.
PR 18-OCT-1995; 95US-0005385P.
PR 05-APR-1996; 96US-00628455.
XX
XX (CHIR) CHIRON CORP.
PA Wernette-Hammond ME, Shyamala V, Siani M, Blaney J;
XX

PI Tekamp-Olson P;
XX WPI; 1997-087095/08.
DR New mutant interleukin-8 poly:peptide(s) - used for modulating
XX interleukin-8 receptor-mediated biological responses.
PT Claim 1; Page 34; 40pp; English.
XX
XX The sequences given in AAW25701-14 represent interleukin-8 (IL-8) mutants
CC which are capable of binding to IL-8 receptors. They can be used for
CC modulating an IL-8 receptor-mediated biological response. The mutations
CC were introduced into the human IL-8 coding sequence by overlap PCR
XX
SQ Sequence 72 AA;
Query Match 73.7%; Score 288; DB 2; Length 72;
Best Local Similarity 76.1%; Pred. No. 1.7e-25;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY 2 ELRCQCIRHTSTPHPKFIFKELRVIESPPHCENSEIIVKLTNGNEVCLNPKRKWQVQ 61
DB 4 ELRCQCIRHTSTPHPKFIFKELRVIESPPHCENSEIIVKLTNGNEVCLNPKRKWQVQ 63
QY 62 VFVKRAE 68
DB 64 KFLKRAE 70
RESULT 13
AAW25705
ID AAW25705 standard; protein; 72 AA.
XX AAW25705;
AC 17-OCT-1997 (first entry)
XX
DT Mutant human IL-8, R47K, E48K, D52N.
XX
DE Interleukin-8; IL-8; IL-8 receptor-mediated biological response; mutant;
KM IL-8 receptor; overlap PCR.
XX
KW Homo sapiens.
XX
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 47 /label= R47K
FT Misc-difference 48 /label= E48K
FT Misc-difference 52 /label= D52N
FT
XX
PN WO9700601-A2.
XX
PD 09-JAN-1997.
XX
PF 18-JUN-1996; 96WO-US010537.
XX
XX 20-JUN-1995; 95US-0002774P.
PR 18-OCT-1995; 95US-0005385P.
PR 05-APR-1996; 96US-00628455.
XX
XX (CHIR) CHIRON CORP.
PA Wernette-Hammond ME, Shyamala V, Siani M, Blaney J;
PI Tekamp-Olson P;
XX WPI; 1997-087095/08.
XX New mutant interleukin-8 poly:peptide(s) - used for modulating
PT interleukin-8 receptor-mediated biological responses.
XX
PS Claim 1; Page 34; 40pp; English.

XX The sequences given in AAW5701-14 represent interleukin-8 (IL-8) mutants
 CC which are capable of binding to IL-8 receptors. They can be used for
 CC modulating an IL-8 receptor-mediated biological response. The mutations
 CC were introduced into the human IL-8 coding sequence by overlap PCR
 XX

Sequence 72 AA;

Query Match 73.7%; Score 288; DB 2; Length 72;
 Best Local Similarity 76.1%; Pred. No. 1.7e-25;
 Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 2 ELRCOCIRTHSTPFHPKFKELRVIESPCHENSEIIVKLTNGNEVCLNPKKRWQKVVQ 61
 Db 4 ELRCOCIKTYSKPFHPKFKELRVIESGPHCANTETIIVKLSGKCLCNPKKNWQKRV 63

QY 62 VFVKRAE 68
 Db 64 KFLKRAE 70

RESULT 14

ABG30773 standard; protein; 71 AA.

ABG30773;

05-NOV-2002 (first entry)

11IP complex polypeptide structure.

XX Cytokine; immune disorder; autoimmune disease; 11IP; interleukin 8; IL-8;
 KM inflammatory disorder; allergy; rhinitis; neoplastic disorder; tumour;
 KM haematological disease; myeloproliferative disorder; Hodgkin's disease;
 KW osteoporosis; obesity; diabetes; gout; cardiovascular disease; AIDS;
 KW reperfusion injury; atherosclerosis; ischaemic heart disease; stroke;
 KW cardiac failure; liver disease; neurological disorder; male infertility;
 KM acquired immunodeficiency syndrome; ageing; bacterial infection; cancer;
 KM viral infection; cytomegalovirus.

OS Unidentified.

PN W0200229062-A2.

PD 11-APR-2002.

PF 04-OCT-2001; 2001WO-GB004412.

PR 04-OCT-2000; 2000GB-00024283.

PA (IMPH-) IMPHARMATICA LTD.

PI Fagan RJ, Phelps CB, Gutteridge A;

DR WPI; 2002-590419/63.

XX Novel cytokine polypeptides useful for treating immune disorders e.g.
 PT autoimmune disease, rheumatoid arthritis, osteoarthritis, inflammatory
 PT disorders, dermatological disease, neoplastic disorders and AIDS.

PS Example 1; Fig 8; 86pp; English.

XX The invention relates to a cytokine polypeptide (C01 or C02), termed
 CC AAW5885.1 and AAW5894.1, and its associated polynucleotide. The
 CC sequences are useful for the treatment of a disease selected from immune
 CC disorders such as autoimmune disease, rheumatoid arthritis,
 CC osteoarthritis, psoriasis, systemic lupus erythematosus, and multiple
 CC sclerosis, inflammatory disorders such as allergy, rhinitis,
 CC conjunctivitis, glomerulonephritis, uveitis, Crohn's disease, ulcerative
 CC colitis, inflammatory bowel disease, pancreatitis, digestive system
 CC inflammation, sepsis, endotoxic shock, septic shock, cachexia, myalgia,
 CC ankylosing spondylitis, myasthenia gravis, post-viral fatigue syndrome,
 CC pulmonary disease, respiratory distress syndrome, asthma, wound healing,

CC chronic-obstructive pulmonary disease, airway inflammation,
 CC endometriosis, dermatological disease, Behcet's disease, neoplastic
 CC disorders such as melanoma, sarcoma, renal tumour, colon tumour,
 CC haematological disease, myeloproliferative disorder, Hodgkin's disease,
 CC osteoporosis, obesity, diabetes, gout, cardiovascular disorders,
 CC reperfusion injury, atherosclerosis, ischaemic heart disease, cardiac
 CC failure, stroke, liver disease, AIDS, AIDS related complex, neurological
 CC disorders, male infertility, ageing and bacterial infections including
 CC plasmidium infection or viral infection, particularly human herpesvirus 5
 CC (cytomegalovirus) infection. This sequence represents an interleukin 8
 CC (IL-8) dimer in complex with a fragment of the IL-8 receptor, used in the
 CC scope of the invention. The complex structure is termed the 11IP
 CC polypeptide

Sequence 71 AA;

Query Match 73.4%; Score 287; DB 5; Length 71;
 Best Local Similarity 76.1%; Pred. No. 2.2e-25;
 Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 2 ELRCOCIRTHSTPFHPKFKELRVIESPCHENSEIIVKLTNGNEVCLNPKKRWQKVVQ 61
 Db 3 ELRCOCIKTYSKPFHPKFKELRVIESGPHCANTETIIVKLSGKCLCNPKKNWQKRV 62

QY 62 VFVKRAE 68
 Db 63 KFLKRAE 69

RESULT 15

AAAP81838 standard; peptide; 72 AA.

AAAP81838;

25-MAR-2003 (revised)

10-MAR-2003 (revised)

17-DEC-2001 (revised)

07-NOV-1990 (first entry)

DE Sequence of a synthetic neutrophil chemotactic polypeptide (NCF).

KM Inflammation; anti-neutrophil chemotactic polypeptide antibody.

OS Homo sapiens.

PN USN7169033-N.

PD 27-SEP-1998.

PF 16-MAR-1988; 88US-00169033.

PR 16-MAR-1988; 88US-00169033.

PA (USSH) US DEPT HEALTH & HUMAN SERVICE.

PI (USDC) US SEC OF COMMERCE.

DR Matushima K, Yoshimur T, Leonard EJ, Oppenheimer J, Appella E;

XX WPI; 1988-322571/45.

XX Synthetic neutrophil chemotactic factor - and its monoclonal antibodies
 PT useful for treating inflammatory conditions.

PS Claim 1; Page 8; 11pp; English.

XX The claimed NCF is composed in whole or in part of the AA sequence in
 CC AAW90913. Anti-NCF MAbs are useful for treating inflammatory conditions.
 CC (Note: Revised entry submitted to correct the patent number format of US
 CC Government-owned NWS applications to prevent clashes with ongoing US
 CC granted patent numbers. For further information please visit the Derwent
 CC web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 10-

CC MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 72 AA;

Query Match 73.4%; Score 287; DB 1; Length 72;
 Best Local Similarity 76.1%; Pred. No. 2.2e-25;
 Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 QY 2 ELRCOCIRHSTPEHPKFKELRVIESPPHCENSEIIVKLTNGNEVCINPEKXWQKVVQ 61
 Db 4 ELRCOCIKTKYSKPFHPKFKELRVIESGPHCANTEIIVKLSDERELCLDPKENWVGRVVE 63
 QY 62 VFVKRAE 68
 Db 64 KFLKRAE 70

Search completed: December 13, 2004, 19:49:13
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OM protein - protein search, using sw model

Run on: December 13, 2004, 19:52:49 ; Search time 144 Seconds

(Without alignments)
178.589 Million cell updates/sec

Title: US-10-087-273-1

Perfect score: 391
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Sequence:

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PTC_NEW_PUB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10E_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10F_NEW_PUB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	391	100.0	72	US-10-087-273-1	Sequence 1, Appl1
2	379	96.9	74	US-10-087-273-2	Sequence 2, Appl1
3	324	82.9	103	US-09-229-304-9	Sequence 9, Appl1
4	287	73.4	72	US-09-811-162-5	Sequence 5, Appl1
5	287	73.4	72	US-10-037-218A-2	Sequence 2, Appl1
6	287	73.4	72	US-10-668-733-13	Sequence 13, Appl1
7	287	73.4	72	US-10-668-733-18	Sequence 18, Appl1
8	287	73.4	72	US-10-803-960-16	Sequence 16, Appl1
9	287	73.4	73	US-10-207-330-26	Sequence 26, Appl1
10	287	73.4	76	US-10-104-755-79	Sequence 79, Appl1
11	287	73.4	77	US-09-792-793A-19	Sequence 19, Appl1
12	287	73.4	77	US-09-811-162-4	Sequence 4, Appl1
13	287	73.4	77	US-10-375-209A-19	Sequence 19, Appl1

14	287	73.4	77	US-10-332-038A-22	Sequence 22, Appl1
15	287	73.4	77	US-10-243-795-1	Sequence 1, Appl1
16	287	73.4	79	US-09-229-304-8	Sequence 8, Appl1
17	287	73.4	9	US-08-927-939-23	Sequence 23, Appl1
18	287	73.4	99	US-09-881-353-175	Sequence 175, Appl1
19	287	73.4	99	US-10-121-113-3	Sequence 3, Appl1
20	287	73.4	99	US-10-099-007A-4	Sequence 4, Appl1
21	287	73.4	99	US-10-104-755-3	Sequence 3, Appl1
22	287	73.4	99	US-10-171-311-93	Sequence 93, Appl1
23	287	73.4	99	US-10-235-994-6	Sequence 6, Appl1
24	287	73.4	99	US-10-301-822-87	Sequence 87, Appl1
25	287	73.4	99	US-10-170-385-251	Sequence 251, Appl1
26	287	73.4	99	US-10-295-027-1209	Sequence 1209, Appl1
27	287	73.4	99	US-10-295-027-1209	Sequence 187, Appl1
28	287	73.4	99	US-10-440-464-183	Sequence 183, Appl1
29	287	73.4	99	US-10-188-832-62	Sequence 62, Appl1
30	287	73.4	99	US-10-734-564-74	Sequence 74, Appl1
31	287	73.4	99	US-10-733-878-511	Sequence 511, Appl1
32	280	71.6	76	US-10-104-755-83	Sequence 83, Appl1
33	279	71.4	76	US-10-104-755-81	Sequence 81, Appl1
34	263	67.3	91	US-09-755-665-48	Sequence 48, Appl1
35	263	67.3	91	US-09-755-665-50	Sequence 50, Appl1
36	263	67.3	91	US-10-629-248-48	Sequence 48, Appl1
37	263	67.3	91	US-10-629-248-50	Sequence 50, Appl1
38	193	49.4	86	US-09-811-162-2	Sequence 2, Appl1
39	193	49.4	103	US-10-121-113-1	Sequence 1, Appl1
40	179	45.8	98	US-10-115-479-24	Sequence 24, Appl1
41	161.5	41.3	72	US-10-115-479-24	Sequence 1, Appl1
42	161.5	41.3	96	US-09-771-023-9	Sequence 9, Appl1
43	148.5	38.0	132	US-09-764-898-258	Sequence 258, Appl1
44	148.5	38.0	132	US-09-764-803-53	Sequence 53, Appl1
45	148.5	38.0	132	US-09-764-877-2055	Sequence 2055, Appl1

ALIGNMENTS

RESULT 1
US-10-087-273-1
Sequence 1, Application US/10087273
Publicat ion No. US20030077705A1
GENERAL INFORMATION:
APPLICANT: Gordon, John R.
APPLICANT: Li, Fang
TITLE OF INVENTION: HIGH-AFFINITY ANTAGONISTS OF EUR-CXC CHEMOKINES
FILE REFERENCE: 47957
CURRENT APPLICATION NUMBER: US/10/087,273
CURRENT FILING DATE: 2002-08-23
PRIOR APPLICATION NUMBER: US 60/273,181
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 72
TYPE: PRT
ORGANISM: Bos taurus
US-10-087-273-1

Query Match 100.0%; Score 391; DB 14; Length 72;
Best Local Similarity 100.0%; Pred. No. 6.6e-38;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TELRCQCFIRTHSTPFHPKFIKEKLVIESPPHCNSSEIIVLTNGNEVCINPKERKQKV 60
DB 1 TELRCQCFIRTHSTPFHPKFIKEKLVIESPPHCNSSEIIVLTNGNEVCINPKERKQKV 60
QY 61 QVFKRAEKQDP 72
DB 61 QVFKRAEKQDP 72
RESULT 2
US-10-087-273-2

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; Sequence 2, Application US/10087273
; Publication No. US20030077705A1
; GENERAL INFORMATION:
; APPLICANT: Gordon, John R.
; APPLICANT: Li, Fang
; TITLE OF INVENTION: HIGH-AFFINITY ANTAGONISTS OF EDR-CXC CHEMOKINES
; FILE REFERENCE: 47957
; CURRENT APPLICATION NUMBER: US/10/087,273
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US 60/273,181
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Bos taurus
; US-10-087-273-2
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Best Local Similarity 97.2%; Pred. No. 1.7e-36;
Matches 70; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Db 3 TELRCOCIRHTSTPFHPKFIKELRVIESGPHCENSEIIVKLTNGNEVCINPKKRWQKVV 62
QY 61 QVFVKRAEKODP 72
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Db 63 QVFVKRAEKODP 74
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RESULT 3
US-09-229-304-9
; Sequence 9, Application US/09229304
; Patent No. US20020090671A1
; GENERAL INFORMATION:
; APPLICANT: TAM, Cheek Shing
; TITLE OF INVENTION: BONE STIMULATING FACTOR
; FILE REFERENCE: 079997/0123
; CURRENT APPLICATION NUMBER: US/09/229,304
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/048,058
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: PCT/CA96/00653
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Porcine
; US-09-229-304-9
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Query Match          82.9%; Score 324; DB 9; Length 103;
Best Local Similarity 87.0%; Pred. No. 6.5e-30;
Matches 60; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
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Db 31 ELRCOCIRHTSTPFHPKFIKELRVIESGPHCENSEIIVKLTNGNEVCINPKKRWQKVVQ 90
QY 62 VFKVRAEKQ 70
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Db 91 IFLKRTKQ 99
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RESULT 4
US-09-811-162-5
; Sequence 5, Application US/09811162
; Publication No. US20030040109A1
; GENERAL INFORMATION:
; APPLICANT: Martins-Green, Manuela
```

```
; APPLICANT: Feugeate, Jo Ellen
; APPLICANT: Li, Qiting
; TITLE OF INVENTION: Chemokines and Methods for Inducing the Differentiation of Fibroblasts
; FILE REFERENCE: 4078-000500US
; CURRENT APPLICATION NUMBER: US/09/811,162
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-811-162-5
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Query Match          73.4%; Score 287; DB 10; Length 72;
Best Local Similarity 76.1%; Pred. No. 8.9e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
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Db 4 ELRCOCIRHTSTPFHPKFIKELRVIESGPHCANTETIIVKLTNGNEVCINPKKRWQKVV 63
QY 62 VFKVRAE 68
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Db 64 KFLKRAE 70
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RESULT 5
US-10-037-218A-2
; Sequence 2, Application US/10037218A
; Publication No. US20020151706A1
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Yoshimura, Teizo
; APPLICANT: Leonard, Edward
; APPLICANT: Openheim, Joost
; APPLICANT: Appella, Ettore
; APPLICANT: Showalter, Stephen
; TITLE OF INVENTION: NOVEL NEUTROPHIL CHEMOTACTIC FACTOR, CLONED cDNA AND MONOCLONAL
; FILE REFERENCE: 2026-4052US4
; CURRENT APPLICATION NUMBER: US/10/037,218A
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 08/818,631
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: US 07/169,033
; PRIOR FILING DATE: 1988-03-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 72
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-037-218A-2
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Query Match          73.4%; Score 287; DB 13; Length 72;
Best Local Similarity 76.1%; Pred. No. 8.9e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
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Db 4 ELRCOCIRHTSTPFHPKFIKELRVIESGPHCANTETIIVKLTNGNEVCINPKKRWQKVV 63
QY 62 VFKVRAE 68
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Db 64 KFLKRAE 70
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RESULT 6
US-10-668-733-13
; Sequence 13, Application US/10668733
; Publication No. US20040138422A1
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; GENERAL INFORMATION:
; APPLICANT: Demotz et al.
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
; FILE REFERENCE: 29964/38772A
; CURRENT APPLICATION NUMBER: US/10/668,733
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 60/412,866
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: msc feature
; LOCATION: (71)..(71)
; OTHER INFORMATION: The amino acid at position 71 is Dpr(Ser) linked to AlexaFluor647
US-10-668-733-13
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Query Match          73.4%; Score 287; DB 16; Length 72;
Best Local Similarity 76.1%; Pred. No. 8.9e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
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DB 4 ELRCQCIKRTSKPHPHFKIKELRVIESGPHCANTETIIVKLSGRELCLDPKENVVQKRVVE 63
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QY 62 VFVGRAR 68
DB 64 KFLKRAE 70
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RESULT 7

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US-10-668-733-18
; Sequence 18, Application US/10668733
; Publication No. US20040138422A1
; GENERAL INFORMATION:
; APPLICANT: Demotz et al.
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
; FILE REFERENCE: 29964/38772A
; CURRENT APPLICATION NUMBER: US/10/668,733
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 60/412,866
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-668-733-18
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Query Match          73.4%; Score 287; DB 16; Length 72;
Best Local Similarity 76.1%; Pred. No. 8.9e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
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QY 2 ELRCQCIKRTSTPHPHFKIKELRVIESPPHCENSEIIVKLTNGNEVCILNPKKKVQKVVQ 61
DB 4 ELRCQCIKRTSKPHPHFKIKELRVIESGPHCANTETIIVKLSGRELCLDPKENVVQKRVVE 63
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QY 62 VFVGRAR 68
DB 64 KFLKRAE 70
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RESULT 8
US-10-803-960-16
; Sequence 16, Application US/10803960
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; Publication No. US20040156822A1
; GENERAL INFORMATION:
; APPLICANT: White, John R.
; APPLICANT: Pelus, Louis
; APPLICANT: Li, Haodong
; APPLICANT: Kreider, Brent L.
; TITLE OF INVENTION: Novel Chemokine for Mobilizing Stem Cells
; FILE REFERENCE: PP497D2
; CURRENT APPLICATION NUMBER: US/10/803,960
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 09/567,225
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/225,501
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: US 60/006,051
; PRIOR FILING DATE: 1995-10-24
; PRIOR APPLICATION NUMBER: US 08/740,033
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 72
; TYPE: PRT
; ORGANISM: NAB-1/IL-8
US-10-803-960-16
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Query Match          73.4%; Score 287; DB 16; Length 72;
Best Local Similarity 76.1%; Pred. No. 8.9e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
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DB 4 ELRCQCIKRTSKPHPHFKIKELRVIESGPHCANTETIIVKLSGRELCLDPKENVVQKRVVE 63
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QY 62 VFVGRAR 68
DB 64 KFLKRAE 70
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RESULT 9

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US-10-207-330-26
; Sequence 26, Application US/10207330
; Publication No. US20030018169A1
; GENERAL INFORMATION:
; APPLICANT: Kochendoerfer, Gerd G
; APPLICANT: Hunter, Christie L
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Botli, Paolo
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
; FILE REFERENCE: gfn-028/02WO
; CURRENT APPLICATION NUMBER: US/10/207,330
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/384,302
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/144,964
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 09/263,971
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-207-330-26
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Query Match          73.4%; Score 287; DB 14; Length 73;
Best Local Similarity 76.1%; Pred. No. 9.1e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
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DB 4 ELRCOCIKITYSKPFHPKFIKELRVIESGPHCANTETIIVKLSDBRELCLDPKKNWQRYVE 63
QY 62 VFVKRAE 68
DB 64 KFLKRAE 70

RESULT 10
US-10-104-755-79

Sequence 79, Application US/10104755
Publication No. US20030031645A1
GENERAL INFORMATION:
APPLICANT: Strieter, Robert M.
Kunkel, Steven L.
TITLE OF INVENTION: CXCL Chemokines as Regulators of Angiogenesis
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,755
FILING DATE: 21-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/213,383
FILING DATE: 09-Dec-1998
APPLICATION NUMBER: 08/468,819
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UMIC:003/HYL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-10-104-755-79

Query Match 73.4%; Score 287; DB 14; Length 76;
Best Local Similarity 76.1%; Pred. No. 9.5e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 2 ELRCOCIRHTSTPHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCINPKKRWQYVQ 61
DB 8 ELRCOCIKITYSKPFHPKFIKELRVIESGPHCANTETIIVKLSDBRELCLDPKKNWQRYVE 67
QY 62 VFVKRAE 68
DB 68 KFLKRAE 74

RESULT 11
US-09-792-793A-19
Sequence 19, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
COGGINS, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 77
TYPE: PRT
ORGANISM: homo sapien
FEATURE:
OTHER INFORMATION: Human Chemokine Polypeptide: Interleukin-8 (IL-8)
US-09-792-793A-19

Query Match 73.4%; Score 287; DB 9; Length 77;
Best Local Similarity 76.1%; Pred. No. 9.6e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 2 ELRCOCIRHTSTPHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCINPKKRWQYVQ 61
DB 9 ELRCOCIKITYSKPFHPKFIKELRVIESGPHCANTETIIVKLSDBRELCLDPKKNWQRYVE 68

QY 62 VFVKRAE 68
DB 69 KFLKRAE 75

RESULT 12
US-09-811-162-4
Sequence 4, Application US/09811162
Publication No. US20030040109A1
GENERAL INFORMATION:
APPLICANT: Martins-Green, Manuela
APPLICANT: Feugate, Jo Ellen
APPLICANT: Li, Qidong
TITLE OF INVENTION: Chemokines and Methods for Inducing the Differentiation of Fibroblasts
FILE REFERENCE: 407E-000500US
CURRENT APPLICATION NUMBER: US/09/811,162
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 77
TYPE: PRT
ORGANISM: Homosapiens
US-09-811-162-4

Query Match 73.4%; Score 287; DB 10; Length 77;
Best Local Similarity 76.1%; Pred. No. 9.6e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 2 ELRCOCIRHTSTPHPKFIKELRVIESPPHCENSEIIVKLTNGNEVCINPKKRWQYVQ 61
DB 9 ELRCOCIKITYSKPFHPKFIKELRVIESGPHCANTETIIVKLSDBRELCLDPKKNWQRYVE 68
QY 62 VFVKRAE 68
DB 69 KFLKRAE 75

RESULT 13
US-10-375-209A-19
Sequence 19, Application US/10375209A
Publication No. US20030215421A1

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; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Cogging, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; FILE REFERENCE: 25020-601E
; CURRENT APPLICATION NUMBER: US/10/375,209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 77
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: Interleukin-8 (IL-8)
US-10-375-209A-19
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Query Match      73.4%; Score 287; DB 14; Length 77;
Best Local Similarity 76.1%; Pred. No. 9.6e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
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QY 2 ELRCQCIKRTSTPFPKPKFKELRVIESPPHCENSEIIVKLTNGNEVCINPKPKKWKQKVVQ 61
DB 9 ELRCQCIKRTSKPFPKPKFKELRVIESGPHCANTETIIVKLSGRELCLDPKKNWVQRVVE 68
QY 62 VFVKRAE 68
DB 69 KFLKRAE 75
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RESULT 14
US-10-332-038A-22
; Sequence 22, Application US/10332038A
; Publication No. US20040077835A1
; GENERAL INFORMATION:
; APPLICANT: Gryphon Therapeutics, Inc.
; APPLICANT: Offord, Robin
; APPLICANT: Gaertner, Hubert
; APPLICANT: Hartley, Oliver
; TITLE OF INVENTION: Chemokine Receptor Modulators, Production and Use
; FILE REFERENCE: 03504.271
; CURRENT APPLICATION NUMBER: US/10/332,038A
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: US 60/217,683
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-332-038A-22
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Query Match      73.4%; Score 287; DB 15; Length 77;
Best Local Similarity 76.1%; Pred. No. 9.6e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
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QY 2 ELRCQCIKRTSTPFPKPKFKELRVIESPPHCENSEIIVKLTNGNEVCINPKPKKWKQKVVQ 61
DB 9 ELRCQCIKRTSKPFPKPKFKELRVIESGPHCANTETIIVKLSGRELCLDPKKNWVQRVVE 68
QY 62 VFVKRAE 68
DB 69 KFLKRAE 75
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RESULT 15
US-10-243-795-1
; Sequence 1, Application US/10243795
; Publication No. US20040197303A1
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
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; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-243-795-1
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Query Match      73.4%; Score 287; DB 17; Length 77;
Best Local Similarity 76.1%; Pred. No. 9.6e-26;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
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QY 2 ELRCQCIKRTSTPFPKPKFKELRVIESPPHCENSEIIVKLTNGNEVCINPKPKKWKQKVVQ 61
DB 9 ELRCQCIKRTSKPFPKPKFKELRVIESGPHCANTETIIVKLSGRELCLDPKKNWVQRVVE 68
QY 62 VFVKRAE 68
DB 69 KFLKRAE 75
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Search completed: December 13, 2004, 20:05:06
Job time : 148 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 19:43:47 ; Search time 38 Seconds

(without alignments)
182.305 Million cell updates/sec

Title: US-10-087-273-1

Perfect score: 391

Sequence: 1 TELRCQCIRHTSTPFPKFI.....EKVQKVQVFKRAEKQDP 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361	92.3	101	S42496	interleukin-8 prec
2	335	85.7	103	A53096	interleukin-8 prec
3	330	84.4	101	I46871	interleukin-8 - ra
4	318	81.3	95	JN0841	interleukin-8 - do
5	287	73.4	99	A37034	interleukin-8 prec
6	280	71.6	101	I48148	Neutrophil attract
7	193	49.4	103	I50417	RSV-induced protei
8	193	49.4	103	A26736	transformation-ind
9	165.5	42.3	117	B44253	alveolar macrophag
10	161.5	41.3	96	A32954	gro-alpha precursor
11	161.5	41.3	101	B28414	growth-regulated p
12	154.5	39.5	96	JN0572	neutrophil chemo-a
13	148.5	38.0	75	B54188	granulocyte chemot
14	145.5	37.2	107	A28414	melanoma growth-st
15	144.5	37.0	107	JH0281	macrophage inflam
16	144.5	37.0	114	A55010	neutrophil-activat
17	142.5	36.4	107	B38280	GRO-gamma precursor
18	138.5	35.4	75	A54188	granulocyte chemot
19	138.5	35.4	128	IGHU	beta-2-microglobul
20	137.5	35.2	132	A57325	C-X-C chemokine li
21	136.5	34.9	100	I55614	macrophage inflam
22	136.5	34.9	100	S21467	cytokine-induced n
23	135.5	34.7	100	S46198	macrophage inflam
24	130.5	33.4	100	JH0200	platelet basic pro
25	127.5	32.6	119	S42881	platelet factor 4,
26	125	32.0	126	A35766	interferon gamma-1
27	124	31.7	90	JN0470	platelet factor 4
28	123.5	31.6	90	S69133	platelet factor 4
29	121	30.9	105	A26774	platelet factor 4

30	118	30.2	53	164831	Gene KC protein -
31	115.5	29.5	101	PFH04	platelet factor 4
32	114.5	29.3	104	PFH04A	platelet factor 4
33	112.5	28.8	98	IGHUG1	interferon gamma-1
34	110	28.1	53	I51886	macrophage inflam
35	108.5	27.7	98	I59277	Mob-1 - rat
36	103.5	26.5	98	A45492	IP-10 precursor -
37	101.5	26.0	113	UC7800	neutrophil activat
38	91.5	23.4	88	PF804	platelet factor 4
39	87	22.3	89	I53416	interleukin-8 homo
40	87	22.3	93	A53497	pre-B-cell growth-
41	87	22.3	93	I81182	cytokine - mouse
42	86	22.0	93	G01540	cytokine SDF-1-bet
43	81	20.7	99	A39296	monocyte chemoatr
44	81	20.7	99	UC2336	monocyte chemoatr
45	80.5	20.6	36	S17507	cytokine - rabbit

ALIGNMENTS

RESULT 1
S42496
interleukin-8 precursor [similarity] - sheep
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S42496; I46997
R/Legislation: I.; Greenland, T.; Arnaud, P.; Mornex, J.F.; Cordier, G.
submitted to the EMBL Data Library, March 1994
A/Description: Nucleotide sequence of ovine interleukin 8 cDNA using polymerase chain r
A/Reference number: S42496
A/Accession: S42496
A/Molecule type: mRNA
A/Residues: 1-101 <LEG>
A/Cross-references: UNIPROT:P36925; EMBL:X78306; NID:G463253; PIDN:CAA55115.1; PID:G463
R/Seq: H.F.; Yoshimura, T.; Wood, P.R.; Colditz, I.G.
Immunol. Cell Biol. 72, 398-405, 1994
A/Title: Cloning, sequencing, expression and inflammatory activity in skin of ovine int.
F/1-20/Domain: signal sequence #status predicted <SIG>
A/Accession: I46997; MUID:95137691; PMID:7835984
A/Status: preliminary; translated from GB/EWBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-101 <SEO>
A/Cross-references: GB:S74436; NID:G786590; PIDN:AA83241.1; PID:G786591
C/Genetics:
A/Gene: IL-8
C/Superfamily: beta-thromboglobulin
C/Keywords: chemotaxis; cytokine; inflammation
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-101/Product: interleukin-8 #status predicted <Mat>

Query Match 92.3%; Score 361; DB 2; Length 101;
Best local Similarity 91.7%; Pred. No. 1.5e-33;
Matches 66; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TELRCQCIRHTSTPFPKFIKEIRVTSPPHCENSEIIVLTNGNEVCLNPKKQKV 60
DB 30 TELRCQCIRHTSTPFPKFIKEIRVTSPPHCENSEIIVLTNGKEVCLDPKQKV 89
QY 61 QVFKRAEKQDP 72
DB 90 QVFKRAEKQDP 101

RESULT 2
A53096
interleukin-8 precursor - pig
N/Alternate names: alveolar macrophage chemotactic factor-I (AMCF-I)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C/Accession: A53096; A44253
R/In: G.; Pearson, A.E.; Scamirra, R.W.; Zhou, Y.; Baarsch, M.J.; Weiss, D.J.; Murtaugh,
J. Biol. Chem. 269, 77-85, 1994

A/Title: Regulation of interleukin-8 expression in porcine alveolar macrophages by bact
 A/Reference number: A53096; MUID:94103307; PMID:8276881
 A/Accession: A53096
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-103 <LIN>
 A/Cross-references: UNIPROT:P26894; GB:M86923; NID:G164520; PIDN:AAA1616.1; PID:G164521
 Biochem. J. 31, 10483-10490, 1992
 A/Note: the sequence in Genbank entry PIGMCF1, release 117.0, has been corrected to cor
 A/Reference number: A44253; MUID:93041741; PMID:1420165
 A/Accession: A44253
 A/Status: preliminary
 A/Molecule type: mRNA; protein
 A/Residues: 1-22, 'D', 24-103 <GOO>
 A/Cross-references: GB:M9367; NID:G1235611
 A/Experimental source: alveolar macrophage
 A/Note: sequence extracted from NCBI backbone (NCBIN:117415, NCBI:P117416)
 A/Note: the sequence in Genbank entry PIGMCF1, release 117.0, has been corrected to cor
 C/Keywords: chemotaxis; cytokines; inflammation
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-103/Product: interleukin-8 #status predicted <MAT>

Query Match 85.7%; Score 335; DB 2; Length 103;
 Best Local Similarity 88.4%; Pred. No. 1.3e-30;
 Matches 61; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 ELRCCGCTHTSPHPKPKIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKKWKVQKV 61
 Db 31 ELRCCGCTHTSPHPKPKIKELRVIESGPHCENSEIIVKLTNGNEVCLNPKKWKVQKV 90

QY 62 VFVKAERKQ 70
 Db 91 IFLKRTKQ 99

RESULT 3

146871
 Interleukin-8 - rabbit
 N/Alternate names: neutrophil attractant/activation protein-1
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
 A/Accession: I46871; S13052
 R/Yoshimura, T.; Yunoki, N.
 J. Immunol. 146, 3483-3488, 1991
 A/Title: Neutrophil attractant/activation protein-1 and monocyte chemoattractant protein
 A/Reference number: I46857; MUID:91225489; PMID:2026877
 A/Accession: I46871
 A/Status: preliminary; translated from GB/EMBL/DBDB
 A/Molecule type: mRNA
 A/Residues: 1-101 <YOS>
 A/Cross-references: UNIPROT:P19874; GB:M57439; NID:G165552; PIDN:AAA31422.1; PID:G16553
 R/Beauchamp, B.C.; Collins, P.D.; Jose, P.J.; Totty, N.F.; Huang, J.; Waterfield, M.D.; W
 Biochem. J. 271, 797-801, 1990
 A/Title: A novel neutrophil chemoattractant generated during an inflammatory reaction in
 Interleukin 8.
 A/Reference number: S13052; MUID:91058518; PMID:2244880
 A/Accession: S13052
 A/Molecule type: protein
 A/Residues: 23-33, 'X', 35, 'X', 37-46, 'X', 48-49, 'I', 51-53 <BEA>
 C/Superfamily: beta-thromboglobulin
 C/Keywords: cytokine

Query Match 84.4%; Score 330; DB 2; Length 101;
 Best Local Similarity 83.1%; Pred. No. 4.5e-30;
 Matches 59; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 TELRCCGCTHTSPHPKPKIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKKWKVQKV 60
 Db 30 TELRCCGCTHTSPHPKPKIKELRVIESGPHCENSEIIVKLTNGNEVCLNPKKWKVQKV 89
 QY 61 QVFVKAERKQD 71

Db 90 QIFLKREKQES 100

RESULT 4

JN0841
 Interleukin-8 - dog
 C/Species: Canis lupus familiaris (dog)
 C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 12-Apr-1995
 A/Accession: JN0841
 R/Rishikawa, Y.; Suzuki, S.; Hotta, K.; Hirota, Y.; Mizuno, S.; Suzuki, K.
 Gene 131, 305-306, 1993
 A/Title: Cloning of a canine gene homologous to the human interleukin-8-encoding gene.
 A/Reference number: JN0841; MUID:94010328; PMID:7916715
 A/Accession: JN0841
 A/Molecule type: DNA
 A/Residues: 1-95 <ISH>
 C/Comment: This protein is a polymorphonuclear leukocytes chemotactic factor and is inv
 C/Genetics:
 A/Intons: 22/1; 67/2
 C/Superfamily: beta-thromboglobulin

Query Match 81.3%; Score 318; DB 2; Length 95;
 Best Local Similarity 84.8%; Pred. No. 9.5e-29;
 Matches 56; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1 TELRCCGCTHTSPHPKPKIKELRVIESPPHCENSEIIVKLTNGNEVCLNPKKWKVQKV 60
 Db 30 SELRCCGCTHTSPHPKPKIKELRVYIDGPHCENSEIIVKLTNGNEVCLNPKKWKVQKV 89

QY 61 QVFVKAERKQ 66
 Db 90 QIFLKREKQ 95

RESULT 5

A37034
 Interleukin-8 precursor - human
 N/Alternate names: beta-thromboglobulin-like protein; fibroblast-derived neutrophil-acti
 te-derived neutrophil chemotactic factor; monocyte-derived neutrophil-activating factor
 C/Species: Homo sapiens (man)
 C/Date: 08-Dec-1992 #sequence_revision 08-Dec-1992 #text_change 09-Jul-2004
 A/Accession: A37034; J10041; A37291; S37634; P10107; A28598; A27488; A39960; A60401; A6C
 J/Mukaido, N.; Shirao, M.; Matsushima, K.
 J. Immunol. 143, 1366-1371, 1989
 A/Title: Genomic structure of the human monocyte-derived neutrophil chemotactic factor i
 A/Reference number: A37034; MUID:89309826; PMID:2663993
 A/Accession: A37034
 A/Molecule type: DNA
 A/Residues: 1-99 <MUK>
 A/Cross-references: UNIPROT:P10145; GB:M28130; NID:G186367; PIDN:AAA59158.1; PID:G18636
 A/Note: the authors failed to translate the last thirty-six nucleotides of the second e
 R/Matsushima, K.; Morishita, K.; Yoshimura, T.; Lavan, S.; Kobayashi, Y.; Lew, W.; Appel
 J. Exp. Med. 167, 1883-1893, 1988
 A/Title: Molecular cloning of a human monocyte-derived neutrophil chemotactic factor (M
 A/Reference number: J10041; MUID:88258376; PMID:3260265
 A/Accession: J10041
 A/Molecule type: mRNA
 A/Residues: 1-99 <MAI>
 A/Cross-references: EMBL:Y00787; NID:G34518; PIDN:CA68742.1; PID:G34519
 A/Note: the sequence shows similarity to several platelet-derived factors, a v-src-induc
 R/Kowalewski, J.; Denhardt, D.T.
 Mol. Cell. Biol. 9, 1946-1957, 1989
 A/Title: Regulation of the mRNA for monocyte-derived neutrophil-activating peptide in di
 A/Reference number: A32791; MUID:89313739; PMID:2664463
 A/Accession: A32791
 A/Molecule type: mRNA
 A/Residues: 1-99 <KOW>
 A/Cross-references: GB:M26383; NID:G186627; PIDN:AAA36333.1; PID:G186628
 R/King, C.H.; Gordon, G.S.; Konieczkowski, M.; Sedor, J.R.
 submitted to the EMBL Data Library, February 1992
 A/Reference number: S37634
 A/Accession: S37634

A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-97 <KIN>
 A/Cross-references: EMBL:Z11686; NID:G33958; PIDN:CAA77745.1; PID:G33959
 R/Suzuki, K.; Miyasaka, H.; Ota, H.; Yamakawa, Y.; Tagawa, M.; Kuramoto, A.; Mizuno, S.
 J. Exp. Med. 169, 1895-1901, 1989
 A/Title: Purification and partial primary sequence of a chemotactic protein for polymorph
 A/Reference number: FL0107; MUID:89279141; PMID:2659722
 A/Accession: FL0107
 A/Molecule type: protein
 A/Residues: 23-32, 'XR', '35', 'X', '37-52', 'L', '54' <SUZ>
 A/Experimental source: lung giant cell carcinoma LU65C
 R/Gregory, H.; Young, J.; Schroeder, J.M.; Mrowietz, U.; Christophers, E.
 Biochem. Biophys. Res. Commun. 151, 883-890, 1988
 A/Title: Structure determination of a human lymphocyte derived neutrophil activating pep
 A/Reference number: A28598; MUID:88162914; PMID:3279957
 A/Accession: A28598
 A/Molecule type: protein
 A/Residues: 28-99 <GRE>
 R/Walz, A.; Fevert, P.; Aschauer, H.; Baggiolini, M.
 Biochem. Biophys. Res. Commun. 149, 755-761, 1987
 A/Title: Purification and amino acid sequencing of NAP, a novel neutrophil-activating fa
 A/Reference number: A27488; MUID:88106502; PMID:3322281
 A/Accession: A27488
 A/Molecule type: protein
 A/Residues: 28-59 <NAL>
 R/Toshimura, T.; Matsushima, K.; Tanaka, S.; Robinson, E.A.; Appella, E.; Oppenheim, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 84, 9233-9237, 1987
 A/Title: Purification of a human monocyte-derived neutrophil chemotactic factor that has
 A/Reference number: A39960; MUID:88097462; PMID:3480540
 A/Accession: A39960
 A/Molecule type: protein
 A/Residues: 28-69 <YOS>
 R/Schroeder, J.M.; Sticherling, M.; Henneicke, H.H.; Preissner, W.C.; Christophers, E.
 J. Immunol. 144, 2223-2232, 1990
 A/Title: IL-1alpha or tumor necrosis factor-alpha stimulate release of three NAP-1/IL-8-
 A/Reference number: A60401; MUID:90187866; PMID:2179408
 A/Accession: A60401
 A/Molecule type: protein
 A/Residues: 23-32 <SCH>
 A/Experimental source: dermal fibroblasts
 A/Note: a minor component of this material (15%) includes an additional two amino acids
 R/Van Damme, J.; Decock, B.; Conings, R.; Lenaerts, J.P.; Opdenacker, G.; Billiau, A.
 Eur. J. Immunol. 19, 1189-1194, 1989
 A/Title: The chemotactic activity for granulocytes produced by virally infected fibrobla
 A/Reference number: A60591; MUID:9338542; PMID:2668011
 A/Accession: A60591
 A/Molecule type: protein
 A/Residues: 23-33, 'X', '35', 'X', '37-42' <VAN>
 R/Nakagawa, H.; Hatakeyama, S.; Ikessue, A.; Miyai, H.
 FEBS Lett. 282, 412-414, 1991
 A/Title: Generation of interleukin-8 by plasmin from AMLP-interleukin-8, the human fibro
 A/Reference number: S15827; MUID:91243843; PMID:1828038
 A/Accession: S15827
 A/Molecule type: protein
 A/Residues: 23-33, 'X', '35', 'X', '37-47' <EB>
 R/Van Damme, J.; van Beeumen, J.; Conings, R.; Decock, B.; Billiau, A.
 Eur. J. Biochem. 181, 337-344, 1989
 A/Title: Purification of granulocyte chemotactic peptide/interleukin-8 reveals N-termin
 A/Reference number: S04216; MUID:9231715; PMID:253801
 A/Accession: S04216
 A/Molecule type: protein
 A/Residues: 21-67 <VAN>
 R/Toshimura, T.; Robinson, E.A.; Appella, E.; Matsushima, K.; Showalter, S.D.; Skeel, A.
 Mol. Immunol. 26, 87-93, 1989
 A/Title: Three forms of monocyte-derived neutrophil chemotactic factor (MNCF) distinguish
 A/Reference number: A60567; MUID:89181632; PMID:2648135
 A/Accession: A60567
 A/Molecule type: protein
 A/Residues: 21-33, 'X', '35', 'X', '37-47' <YO2>
 A/Note: the forms starting from positions 21, 23, and 28 represented 8%, 47%, and 45%, r
 R/Van Damme, J.; Van Beeumen, J.; Opdenacker, G.; Billiau, A.
 J. Exp. Med. 167, 1364-1376, 1988

A/Title: A novel, NH-2-terminal sequence-characterized human monokine possessing neutro
 A/Reference number: A60847; MUID:88187604; PMID:3258625
 A/Accession: A60847
 A/Molecule type: protein
 A/Residues: 28-47 <VA3>
 R/Car, B.D.; Baggiolini, M.; Walz, A.
 Biochem. J. 275, 581-584, 1991
 A/Title: Formation of neutrophil-activating peptide 2 from platelet-derived connective-
 A/Reference number: S15417; MUID:91248085; PMID:2039437
 A/Accession: S15417
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 28-99 <CAR>
 R/Gold, E.E.; Mason, P.; Nyirko, P.
 Biochem. J. 259, 585-588, 1989
 A/Title: Inflammatory cytokines induce synthesis and secretion of GRO protein and a neu
 A/Reference number: S03975; MUID:89246368; PMID:2655583
 A/Accession: S03975
 A/Molecule type: protein
 A/Residues: 23-46 <COL>
 R/Hotta, K.; Hayashi, K.; Ishikawa, J.; Tagawa, M.; Hashimoto, K.; Mizuno, S.; Suzuki, I.
 Immunol. Lett. 24, 165-170, 1990
 A/Title: Coding region structure of interleukin-8 gene of human lung giant cell carcinoma
 A/Reference number: I54560; MUID:90346419; PMID:2200751
 A/Accession: I54560
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-99 <RES>
 A/Cross-references: GB:D14283; NID:G219915; PIDN:BA03245.1; PID:G219916
 R/Schmidt, J.; Weisemann, C.
 J. Immunol. 139, 250-256, 1987
 A/Title: Induction of mRNA for a serine protease and a beta-thromboglobulin-like protea
 A/Reference number: I55992; MUID:87224164; PMID:2953813
 A/Accession: I55992
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-99 <RES>
 A/Cross-references: GB:M17017; NID:G179579; PIDN:AAA5611.1; PID:G179580
 R/Kusner, D.J.; Luebers, E.L.; Nowinski, R.J.; Konieczkowski, M.; King, C.H.; Sedor, J.
 Kidney Int. 39, 1240-1248, 1991
 A/Title: Cytokine- and LPS-induced synthesis of interleukin-8 from human mesangial cell.
 A/Reference number: I37902; MUID:91374977; PMID:1895676
 A/Accession: I37902
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-97 <R3>
 A/Cross-references: EMBL:Z11686; NID:G33958; PIDN:CAA77745.1; PID:G33959
 R/Alouani, S.; Gaertner, H.F.; Mermod, J.U.; Power, C.A.; Bacon, K.B.; Wells, T.N.C.; P
 Eur. J. Biochem. 227, 328-334, 1995
 A/Title: A fluorescent interleukin-8 receptor probe produced by targeted labelling at
 A/Reference number: S67519; MUID:95154308; PMID:7851404
 A/Accession: S67519
 A/Molecule type: mRNA
 A/Residues: 1-99 <ALO>
 C/Comment: This secretory protein is chemotactic for polymorphonuclear leukocytes.
 C/Comment: This protein is variably processed at the amino end. The major form differs
 C/Genetics:
 A/Gene: GDB:118
 A/Cross-references: GDB:120099; OMIM:146930
 A/Map position: 4q13-4q21
 A/Introns: 22/1, 67/2, 95/2
 C/Superfamily: beta-thromboglobulin
 C/Keywords: chemotaxis; cytokine; inflammation
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-99/Product: interleukin-8, minor form #status experimental <MATA>
 F:28-99/Product: interleukin-8, major fibroblast-derived form #status experimental <MAT>
 F:28-99/Product: interleukin-8, major lymphocyte/monocyte-derived form #status experi

Query Match 73.4%; Score 287; DB 2; Length 99;
 Best Local Similarity 76.1%; Pred. No. 3e-25;
 Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 2 ELRGQCRHSTPFFHKFKELRVIESPFCENSEIIVLTGNENVCANPKKRVQKVQ 61

```

Db      31 ELRCQCIKTVSKPFPKFKIKELRVIESGPHCANBIIIVKLSGKELCLDPKKNWQKRV 90
QY      62 VFVKRAE 68
        |||||
Db      91 KFLKRAE 97

```

RESULT 6

```

148148
Neutrophil attractant protein-1 - guinea pig
C/Species: Cavia porcellus (guinea pig)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 148148
R:Yoshimura, T.; Johnson, D.G.
J. Immunol. 151, 6225-6236, 1993
A/Title: cDNA cloning and expression of guinea pig neutrophil attractant protein-1 (NAP-1)
A/Reference number: 148148; MUID:94065176; PMID:7504015
A/Accession: 148148
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-101 <RES>
A/Cross-references: UNIPROT:P49113; GB:L04986; NID:9459764; PIDN:AAA37049.1; PID:9459765
C/Genetics:
A/Genes: NAP-1
C/Superfamily: beta-thromboglobulin

```

```

Query Match      71.6%; Score 280; DB 2; Length 101;
Best Local Similarity 69.0%; Pred. No. 1.3e-24;
Matches 49; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

```

```

QY      1 TELRCQCIKTVSKPFPKFKIKELRVIESGPHCANBIIIVKLTNGNEVCINPKKWKQKVV 60
        |||||
Db      30 ELRCQCIKTVSKPFPKFKIKELRVIESGPHCANBIIIVKLTNGNEVCINPKKWKQKVV 89
QY      61 QVFKRAEKOD 71
        |||||
Db      90 SMFLKRTESQD 100

```

RESULT 7

```

150417
RSV-induced protein - chicken
C/Species: Gallus gallus (chicken)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: 150417
R:Bedard, P.
Proc. Natl. Acad. Sci. U.S.A. 84, 6715-6719, 1987
A/Title: Constitutive expression of a gene encoding a polypeptide homologous to biologic
A/Reference number: 150417; MUID:88016162; PMID:2821543
A/Accession: 150417
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-103 <BED>
A/Cross-references: UNIPROT:P08317; GB:J02975; NID:9212643; PIDN:AAA49059.1; PID:9212644
C/Superfamily: beta-thromboglobulin

```

```

Query Match      49.4%; Score 193; DB 2; Length 103;
Best Local Similarity 50.7%; Pred. No. 1.2e-14;
Matches 34; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

```

```

QY      2 ELRCQCIKTVSKPFPKFKIKELRVIESGPHCANBIIIVKLTNGNEVCINPKKWKQKVV 61
        |||||
Db      30 ELRCQCIKTVSKPFPKFKIKELRVIESGPHCANBIIIVKLTNGNEVCINPKKWKQKVV 89
QY      62 VFVKRAE 68
        |||||
Db      90 ALMAKQ 96

```

RESULT 8

A26736

```

transformation-induced protein precursor (clone 9E3) - chicken
C/Species: Gallus gallus (chicken)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C/Accession: A26736
R:Sugano, S.; Stockle, M.Y.; Hanafusa, H.
Cell 49, 321-328, 1987
A/Title: Transformation by Rous sarcoma virus induces a novel gene with homology to a m
A/Reference number: A26736; MUID:87187628; PMID:3032449
A/Accession: A26736
A/Molecule type: mRNA
A/Residues: 1-103 <SUG>
A/Cross-references: UNIPROT:P08317; GB:M16199; NID:9211735; PIDN:AAA48758.1; PID:9211736
C/Superfamily: beta-thromboglobulin

```

```

Query Match      49.4%; Score 193; DB 2; Length 103;
Best Local Similarity 50.7%; Pred. No. 1.2e-14;
Matches 34; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

```

```

QY      2 ELRCQCIKTVSKPFPKFKIKELRVIESGPHCANBIIIVKLTNGNEVCINPKKWKQKVV 61
        |||||
Db      30 ELRCQCIKTVSKPFPKFKIKELRVIESGPHCANBIIIVKLTNGNEVCINPKKWKQKVV 89
QY      62 VFVKRAE 68
        |||||
Db      90 ALMAKQ 96

```

RESULT 9

```

B44253
alveolar macrophage chemotactic factor-II (AMCF-II) intercrine-alpha protein - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: B44253
R:Goodman, R.B.; Foster, D.C.; Mathewes, S.L.; Osborn, S.G.; Kuiper, J.L.; Forstrom, J
Biochemistry 31, 10483-10490, 1992
A/Title: Molecular cloning of porcine alveolar macrophage-derived neutrophil chemotactic
A/Reference number: A44253; MUID:93041741; PMID:1420165
A/Accession: B44253
A/Status: preliminary
A/Molecule type: mRNA; protein
A/Residues: 1-117 <GOO>
A/Cross-references: UNIPROT:P22952; GB:M99368; NID:9164325; PIDN:AAA30991.1; PID:9164326
A/Experimental source: alveolar macrophage
A/Note: sequence extracted from NCBI backbone (NCBI:117417, NCBI:P:117418)
C/Superfamily: beta-thromboglobulin

```

```

Query Match      42.3%; Score 165.5; DB 2; Length 117;
Best Local Similarity 45.1%; Pred. No. 1.7e-11;
Matches 32; Conservative 14; Mismatches 22; Indels 3; Gaps 2;

```

```

QY      2 ELRCQCIKTVSKPFPKFKIKELRVIESGPHCANBIIIVKLTNGNEVCINPKKWKQKVV 60
        |||||
Db      49 ELRCQCIKTVSKPFPKFKIKELRVIESGPHCANBIIIVKLTNGNEVCINPKKWKQKVV 106
QY      61 QVFKRAEKOD 71
        |||||
Db      107 QKMLDSGRKN 117

```

RESULT 10

A32954

```

gro-alpha precursor - mouse
N/Alternate names: gro protein; growth regulated protein; melanoma growth-stimulating ac
C/Species: Mus musculus (house mouse)
C/Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 09-Jul-2004
C/Accession: A32954; JH0081
R:Quendo, P.; Alberta, U.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.
J. Biol. Chem. 264, 4133-4137, 1989
A/Title: The platelet-derived growth factor-inducible KC gene encodes a secretory protei
A/Reference number: A32954; MUID:89139485; PMID:2917992

```

A/Accession: A32954
 A/Molecule type: mRNA
 A/Residues: 1-96 <OQ>
 A/Cross-references: UNIPROT:P12850; GB:J04596; NID:G201042; PIDN:AAA40131.1; PID:G201043
 R/Rybeck, R.P.; MacDonald-Bravo, H.; Mattei, M.G.; Bravo, R.
 Exp. Cell Res. 180, 266-275, 1989
 A/Title: Cloning and sequence of a secretory protein induced by growth factors in mouse
 A/Reference number: JH0081; MUID:89078502; PMID:2909392
 A/Accession: JH0081
 A/Molecule type: mRNA
 A/Residues: 1-96 <RYS>
 C/Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.
 C/Genetics:
 A/Map position: 5
 C/Superfamily: beta-thromboglobulin
 C/Keywords: extracellular protein
 F/1-24/Domain: signal sequence #status predicted <SIG>
 F/25-96/Product: gro-alpha #status predicted <MAT>

Query Match 41.3%; Score 161.5; DB 2; Length 96;
 Best Local Similarity 47.1%; Pred. No. 3.8e-11;
 Matches 32; Conservative 11; Mismatches 24; Indels 1; Gaps 1;

QY 2 ELRCQCIKTHSTPHPKFKELRYIESPPHCENSEIIYKLTNGNEVCINPKKKVQKVVQ 61
 DB 30 ELRCQCIQCT-MAGIHLKNIOQLKVPSPGPHCTQTEVIATLKNGREACLDPEAPLVQKIVQ 88

QY 62 VFVRAEK 69
 DB 89 KMLKGVPK 96

RESULT 11
 B28414
 growth-regulated protein precursor - Chinese hamster
 C/Species: Cricetus griseus (Chinese hamster)
 C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
 C/Accession: B28414
 R/Andisovic, A.; Bardwell, L.; Sager, R.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987
 A/Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese h
 A/Reference number: A94184; MUID:88041072; PMID:2890161
 A/Accession: B28414
 A/Molecule type: mRNA
 A/Residues: 1-101 <ANI>
 A/Cross-references: UNIPROT:P09340; GB:J03560; NID:G191088; PIDN:AAA36985.1; PID:G304508
 A/Note: the authors translated the codon CAG for residue 52 as Glu
 C/Superfamily: beta-thromboglobulin
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/24-101/Product: growth-regulated protein #status predicted <MAT>

Query Match 41.3%; Score 161.5; DB 2; Length 101;
 Best Local Similarity 50.0%; Pred. No. 4.1e-11;
 Matches 32; Conservative 9; Mismatches 22; Indels 1; Gaps 1;

QY 2 ELRCQCIKTHSTPHPKFKELRYIESPPHCENSEIIYKLTNGNEVCINPKKKVQKVVQ 61
 DB 34 ELRCQCIQCT-MTGVIHLKNIOQLKVPSPGPHCTQTEVIATLKNGREACINPEAPLVQKIVQ 92

QY 62 VFVRAEK 65
 DB 93 KMLK 96

RESULT 12
 JN0572
 neutrophil chemo-attractant Gro protein precursor - rat
 N/Alternate names: CINC, cytokine-induced neutrophil chemotactant; interleukin-8-like
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C/Accession: JN0572; JQ1519; A34481; A48988; B48988; S51214
 R/Konishi, K.; Takata, Y.; Yamamoto, M.; Yomogida, K.; Watanabe, K.; Tsunufuji, S.; Fujii
 Gene 126, 285-286, 1993

A/Title: Structure of the gene encoding rat neutrophil chemo-attractant Gro.
 A/Reference number: JN0572; MUID:93246259; PMID:8482545
 A/Accession: JN0572
 A/Molecule type: DNA
 A/Residues: 1-96 <KON>
 A/Cross-references: UNIPROT:P14095; DDBJ:D11445; NID:G391854; PIDN:BA02009.1; PID:G220
 R/Huang, S.; Paulauktis, J.D.; Kobzik, L.
 Biochem. Biophys. Res. Commun. 184, 922-929, 1992
 A/Title: Rat KC cDNA cloning and mRNA expression in lung macrophages and fibroblasts.
 A/Reference number: JQ1519; MUID:92246987; PMID:1374243
 A/Accession: JQ1519
 A/Molecule type: mRNA
 A/Residues: 1-32, 'S', 34-96 <HUA>
 A/Cross-references: GB:W86536
 A/Experimental source: alveolar macrophage
 A/Note: the authors translated the codon AGT for residue 33 as Cys, AAC for residue 46
 R/Watanabe, K.; Konishi, K.; Fujioaka, M.; Kinoshita, S.; Nakagawa, H.
 J. Biol. Chem. 264, 19559-19563, 1989
 A/Title: The neutrophil chemotactant produced by the rat kidney epithelioid cell lin
 A/Reference number: A34481; MUID:9062049; PMID:2684956
 A/Accession: A34481
 A/Molecule type: protein
 A/Residues: 25-96 <MAT>
 R/Nakagawa, H.; Ikeue, A.; Hatkeyama, S.; Kato, H.; Goroda, T.; Komorita, N.; Watanab
 Biochem. Pharmacol. 45, 1425-1430, 1993
 A/Title: Production of an interleukin-8-like chemokine by cytokine-stimulated rat NRK-4
 A/Reference number: A48988; MUID:93228656; PMID:8471066
 A/Accession: A48988
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 25-57 <NRK>
 A/Experimental source: kidney, NRK-49P fibroblasts
 A/Note: sequence extracted from NCBI backbone (NCBIP:129132)
 A/Accession: B48988
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 25-57 <NRK>
 A/Experimental source: kidney, NRK-49P fibroblasts
 A/Note: sequence extracted from NCBI backbone (NCBIP:129131)
 R/Hanzawa, H.; Haruyama, H.; Watanabe, K.; Tsunufuji, S.
 FEBS Lett. 354, 207-212, 1994
 A/Title: The three dimensional structure of rat cytokine CINC/Gro in solution by homonu
 A/Reference number: S51214; MUID:95046335; PMID:7957925
 A/Accession: S51214
 A/Contents: annotation; conformation by (1)H-NMR, residues 25-96
 A/Residues: 25-96 <HNR>
 C/Comment: This protein has chemotactic activity for neutrophils and has melanoma growt
 C/Genetics:
 A/Gene: gro, KC
 A/Intons: 24/1; 65/2; 92/2
 C/Superfamily: beta-thromboglobulin
 C/Keywords: cytokine; disulfide bond
 F/1-24/Domain: signal sequence #status predicted <SIG>
 F/25-96/Product: neutrophil chemo-attractant Gro protein #status experimental <CYT>

Query Match 39.5%; Score 154.5; DB 2; Length 96;
 Best Local Similarity 45.6%; Pred. No. 2.3e-10;
 Matches 31; Conservative 11; Mismatches 25; Indels 1; Gaps 1;

QY 2 ELRCQCIKTHSTPHPKFKELRYIESPPHCENSEIIYKLTNGNEVCINPKKKVQKVVQ 61
 DB 30 ELRCQCIQCT-VAGIHFNKIOQLKVPSPGPHCTQTEVIATLKNGREACLDPEAPLVQKIVQ 88

QY 62 VFVRAEK 69
 DB 89 KMLKGVPK 96

RESULT 13
 B54188
 granulocyte chemotactic protein, GCP-2 - bovine
 C/Species: Bos primigenius taurus (cattle)

A;Reference number: A60407; MUID:90257367; PMID:2341726
 A;Accession: A60407
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 56-107 <SPO>
 C;Superfamily: beta-chromoglobulin
 C;Keywords: inflammation
 F;1-34/Domain: signal sequence #status predicted <SIG>
 F;35-107/Product: macrophage inflammatory protein 2 alpha #status predicted <MAT>

Query Match 37.0%; Score 144.5; DB 2; Length 107;
 Best local similarity 39.7%; Pred. No. 3.5e-09;
 Matches 27; Conservative 14; Mismatches 26; Indels 1; Gaps 1;

QY	1	TELRCQCI	RTHSTP	PHPKFI	KELVIES	PPHCENSE	IIIVKL	TNGNEV	CLNPK	KEK	VOQ	KV	60
Db	39	TELRCQCI	QIQT	LQGI	HLKNI	QSVK	KS	PGPH	CAQTE	VITAT	LKNG	QKAC	LN
QY	61	QVFYK	RAE										68
Db	98	EKM	LKNG	K									105

Search completed: December 13, 2004, 19:53:18
 Job time : 38 secs

Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 19:35:47 ; Search time 194 Seconds

(without alignments)
213.541 Million cell updates/sec

Title: US-10-087-273-1

Sequence: 1 TEHRCCGICRTHSTPHPKPT.....EKVVQKVQVFKRAEKQDP 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	379	96.3	101	IL8_BOVIN	P79255 bos taurus
2	364	92.9	101	IL8_SHEEP	P36925 ovis aries
3	350	89.5	101	IL8_CANFA	P41324 canis fami
4	345	88.2	101	Q7YRHS	P76894 tursiops tr
5	335	85.7	103	IL8_PIG	P26894 sus scrofa
6	335	85.7	103	BAC06611	BAC06611 sus scro
7	330	84.4	101	IL8_RABIT	P19874 coryctolagus
8	312	79.8	101	IL8_FELCA	Q938X5 felis silve
9	299	76.5	101	IL8_MACMU	P51495 macaca mula
10	286	75.7	101	Q866R3	Q866R3 equus cabal
11	288	73.7	56	Q71UR4	Q71UR4 bos taurus
12	288	73.7	56	AAD02808	AAD02808 bos tauru
13	287	73.4	97	O61AB6	O61AB6 homo sapien
14	287	73.4	97	CAAT7745	CAAT7745 homo sapi
15	287	73.4	99	IL8_HUMAN	P10145 h interleuk
16	287	72.9	99	AAP35730	AAP35730 homo sapi
17	285	72.9	97	IL8_HORSE	O62812 equus cabal
18	284	72.6	101	IL8_CAVRO	P46653 cercocebus
19	280	71.6	101	IL8_CAVRO	P46653 cercocebus
20	258	66.0	61	O61AA1	O61AA1 canis fami
21	258	66.0	61	CAAS3910	CAAS3910 canis fam
22	196	50.1	101	O8UW91	O8UW91 triakis scy
23	193	49.4	103	EMF1_CHICK	EMF1_CHICK gallus gall
24	193	49.4	103	CAB37669	CAB37669 gallus ga
25	192	49.1	104	Q73912	Q73912 gallus gall
26	170	43.5	100	O8AXP4	O8AXP4 chimaera ph
27	165.5	42.3	117	AMC2_PIG	P22932 sus scrofa
28	161.5	41.3	96	GRO_MOUSE	P12850 mus musculu
29	161.5	41.3	101	GRO_CRIGR	P09340 cricetus
30	155.5	39.8	100	Q91ZK9	Q91ZK9 sigmodon hi
31	154.5	39.5	96	GRO_RAT	P14095 ratius norv

ALIGNMENTS

RESULT 1	ID	IL8_BOVIN	STANDARD	PRT	101 AA.	Q6PUD4
AC	P79255					AAS91557
DT	01-NOV-1997 (Rel. 35, Created)					Q6PUJ1
DT	01-NOV-1997 (Rel. 35, Last sequence update)					AAS90943
DT	05-JUL-2004 (Rel. 44, Last annotation update)					AMC_RABIT
DE	Interleukin-8 precursor (IL-8) (CXCL8).					Q91Z64
GN	Name=IL8;					O8HXZ4
OS	Bos taurus (Bovine).					O8HXZ3
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					P80221
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;					Q28724
OC	Bovinae; Bos.					P09341
OX	NCBI_TaxID=9913;					AAP35526
OX	[1]					M12A_HUMAN
RN	SEQUENCE FROM N.A.					SZ05_HUMAN
RX	MEDLINE=96304552; PubMed=8737490;					
RA	Morsey M.A., Popowich Y., Kowaleki J., Gerlach G., Godson D.,					
RA	Campes M., Babluk L.A.;					
RT	Molecular cloning and expression of bovine interleukin-8.;					
RT	Microb. Pathog. 20:203-212(1996).					
RP	SEQUENCE FROM N.A.					
RA	Galligan C.L., Yoshimura T., Coomber B.L.;					
RT	"Cloning and sequencing of bovine interleukin 8 cDNA isolated from					
RT	lipopolysaccharide stimulated monocytes in vitro."					
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.					
CC	-1- FUNCTION: IL-8 is a chemotactic factor that attracts neutrophils,					
CC	basophils, and T-cells, but not monocytes. It is also involved in					
CC	neutrophil activation. It is released from several cell types in					
CC	response to an inflammatory stimulus (By similarity).					
CC	-1- SUBUNIT: Homodimer (By similarity).					
CC	-1- SUBCELLULAR LOCATION: Secreted.					
CC	-1- SIMILARITY: Belongs to the interleukin alpha (chemokine CXC)					
CC	family.					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/					
CC	or send an email to license@isb-sib.ch).					
CC	EMBL; S82598; AAB37483.1; -					
CC	EMBL; AF232704; AAF37575.1; -					
CC	HSSP; P10145; 1IKM.					
DR	GO; GO:0005576; C:extracellular; NAS.					
DR	GO; GO:0005153; F:interleukin-8 receptor binding; IRP.					
DR	GO; GO:0050930; P:induction of positive chemotaxis; IMP.					
DR	GO; GO:0042119; P:neutrophil activation; TAS.					
DR	GO; GO:0030593; P:neutrophil chemotaxis; IMP.					
DR	InterPro; IPR002473; C-X-C/Interlkn_8.					
DR	InterPro; IPR001811; Chemokine_IL8.					

DR InterPro: IPR001089; CXCL chemokine sm1.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS; PR00436; INTERLEUKIN8.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00471; SMALL CYTOKINES CXCL; 1.
 KW Chemotaxis; Cytokine; Inflammatory response; signal.
 FT SIGNAL 1 22 By similarity.
 FT CHAIN 23 101 Interleukin-8.
 FT DISULFID 34 61 By similarity.
 FT DISULFID 36 77 By similarity.
 SQ SEQUENCE 101 AA; 11291 MW; 061A530507906736 CRC64;
 Query Match 96.9%; Score 379; DB 1; Length 101;
 Best Local Similarity 97.2%; Pred. No. 2.3e-35;
 Matches 70; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TELRCOCIRTHSTPHPKFKELRVIESPPHCENSEIIYKLTNGNEVCINPKKWKVQKV 60
 Db 30 TELRCOCIRTHSTPHPKFKELRVIESGPHCENSEIIYKLTNGNEVCINPKKWKVQKV 89
 QY 61 QVFVKRAEKODP 72
 Db 90 QVFVKRAEKODP 101
 RESULT 2
 IL8 SHEEP STANDARD; PRT; 101 AA.
 ID IL8 SHEEP P36925;
 AC 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8).
 GN Name=IL8;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95121931; PubMed=7821808;
 RT "Legatelejois I., Greenand T., Arnaud P., Mornex J.F., Cordier G.;
 RT "Sequencing of the ovine interleukin-8 encoding cDNA using the
 RT polymerase chain reaction.";
 RT Gene 150:367-369 (1994).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95137691; PubMed=7835984;
 RX "Seow H.F., Yoshimura T., Wood P.R., Colditz I.G.;
 RX "Cloning, sequencing, expression and inflammatory activity in skin of
 RX ovine interleukin-8.";
 RL Immunol. Cell Biol. 72:398-405 (1994).
 CC -1- FUNCTION: IL-8 is a chemotactic factor that attracts neutrophils,
 CC basophils, and T-cells, but not monocytes. It is also involved in
 CC neutrophil activation. It is released from several cell types in
 CC response to an inflammatory stimulus.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: Belongs to the interleukin alpha (chemokine Cxcl)
 CC family.
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 CC EMBL; X78306; CAAS5115.1; -
 CC EMBL; S74436; AAB33241.1; -

DR PIR: S42496; S42496.
 DR HSSP; P10145; IIRK.
 DR InterPro: IPR002473; C-X-C/Interln_8.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; CXCL chemokine sm1.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS; PR00436; INTERLEUKIN8.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00471; SMALL CYTOKINES CXCL; 1.
 KW Chemotaxis; Cytokine; Inflammatory response; signal.
 FT SIGNAL 1 22 By similarity.
 FT CHAIN 23 101 Interleukin-8.
 FT DISULFID 34 61 By similarity.
 FT DISULFID 36 77 By similarity.
 SQ SEQUENCE 101 AA; 11292 MW; 40E8418B57C56A5B CRC64;
 Query Match 92.3%; Score 361; DB 1; Length 101;
 Best Local Similarity 91.7%; Pred. No. 2.6e-33;
 Matches 66; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TELRCOCIRTHSTPHPKFKELRVIESPPHCENSEIIYKLTNGNEVCINPKKWKVQKV 60
 Db 30 TELRCOCIRTHSTPHPKFKELRVIESGPHCENSEIIYKLTNGNEVCINPKKWKVQKV 89
 QY 61 QVFVKRAEKODP 72
 Db 90 QVFVKRAEKODP 101
 RESULT 3
 IL8 CANPA STANDARD; PRT; 101 AA.
 ID IL8 CANPA P41324;
 AC 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8).
 GN Name=IL8;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94010328; PubMed=7916715;
 RT "Ishikawa J., Suzuki S., Hotta K., Hirota Y., Mizuno S., Suzuki K.;
 RT "Cloning of a canine gene homologous to the human interleukin-8-
 RT encoding gene.";
 RT Gene 131:305-306 (1993).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Lymph node;
 RX MEDLINE=95127913; PubMed=7827282;
 RA Matsumoto Y., Mohamed A., Onodera T., Kato H., Ohashi T., Goitsuka R.,
 RA Tejumomo H., Hasegawa A., Furusawa S., Yoshihara K., Ishikawa J.,
 RA Hotta K., Suzuki K., Hirota Y.;
 RT "Molecular cloning and expression of canine interleukin 8 cDNA.";
 RT Cytokine 6:455-461 (1994).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Mongrel; TISSUE=Jugular vein;
 RX MEDLINE=95114148; PubMed=7814650;
 RA Kukeleka G.L., Smith W.C., Larosa G.D., Manning A.M., Mendoza L.H.,
 RA Daly T.J., Hughes B.J., Youker K.A., Hawkins H.K., Michael L.H.,
 RA Rot A., Entman M.L.;
 RT "Interleukin-8 gene induction in the myocardium after ischemia and
 RT reperfusion in vivo.";
 RT J. Clin. Invest. 95:89-103 (1995).
 RL [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Beagle;
 RX MEDLINE=97230298; PubMed=9119462;

RA Straubinger R.K., Straubinger A.F., Harter L., Jacobson R.H.,
 RA Chang Y.-F., Summers B.A., Erb H.N., Appel M.J.,
 RT "Borrelia burgdorferi migrates into joint capsules and causes an up-
 regulation of interleukin-8 in synovial membranes of dogs
 RT experimentally infected with ticks.";
 RL Infect. Immun. 65:1273-1285(1997).
 CC -1- FUNCTION: IL-8 is a chemotactic factor that attracts neutrophils,
 CC basophils, and T-cells, but not monocytes. It is also involved in
 CC neutrophil activation. It is released from several cell types in
 CC response to an inflammatory stimulus.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the interleukin alpha (chemokine CXC)
 CC family.
 CC -----
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 CC -----
 CC EMBL; D28772; BAA05961.1; -;
 CC EMBL; D14285; BAA03246.1; -;
 CC EMBL; U10308; AAC48434.1; -;
 CC EMBL; AF048717; AAC05134.1; -;
 CC HSSP; P10145; 1IKM.
 CC InterPro; IPR002473; C-X-C/Interlkn_8.
 CC InterPro; IPR001811; Chemokine IL8_
 CC InterPro; IPR001089; CXC_chemkine_sm1.
 CC Pfam; PF00048; IL8_1.
 CC PRINTS; PR00436; INTERLEUKIN8.
 CC DR PRINTS; PR00437; SMALLCYTCCXC.
 CC SMART; SM00199; SCY; 1.
 CC PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
 CC KEGG; Chemotaxis; Cytokine; Inflammatory response; Signal.
 CC FT SIGNAL 1 22 By similarity.
 CC FT CHAIN 23 101 Interleukin-8.
 CC FT DISULFID 34 61 By similarity.
 CC FT DISULFID 36 77 By similarity.
 CC SQ SEQUENCE 101 AA; 11280 MW; 3A3A4676DA968376 CRC64;
 Query Match 89.5%; Score 350; DB 1; Length 101;
 Best Local Similarity 86.1%; Pred. No. 4.6e-32;
 Matches 62; Conservative 8; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TELRCOCIRTHSPFPHKFKIKELRVIESPPHCENSEIIVKLTNGNEVCINPKKCKVQKV 60
 Db 30 SELRCOCIRTHSPFPHKFKIKELRVIDSPPHCENSEIIVKLTNGNEVCINPKKCKVQKV 89
 QY 61 QVFWKRAEKQDP 72
 Db 90 QIFLKRKQKDP 101
 RESULT 4
 Q7YRB5 PRELIMINARY; PRT; 101 AA.
 AC Q7YRB5;
 DT 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Interleukin-8.
 GN Name=IL-8;
 OS Turbaloops truncatus (Atlantic bottle-nosed dolphin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 OC Turbaloops.
 OX NCBI_TaxID=9739;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP Yosida Y., Shoji Y., Endo T., Ito T., Sakai T.;

RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yoshida Y., Shoji Y., Endo T., Ito T., Sakai T.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB096002; BAC81421.1; -;
 DR GO; GO:0005576; Cxcracellulinar; IEA.
 DR GO; GO:0008009; Fchemokine activity; IEA.
 DR GO; GO:0006955; P:Immune response; IEA.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR InterPro; IPR001089; CXC_chemkine_sm1.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
 SQ SEQUENCE 101 AA; 11370 MW; 2A5DFE251D980E15 CRC64;
 Query Match 88.2%; Score 345; DB 2; Length 101;
 Best Local Similarity 86.1%; Pred. No. 1.7e-31;
 Matches 62; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TELRCOCIRTHSPFPHKFKIKELRVIESPPHCENSEIIVKLTNGNEVCINPKKCKVQKV 60
 Db 30 SELRCOCIRTHSPFPHKFKIKELRVIDSPPHCENSEIIVKLTNGNEVCINPKKCKVQKV 89
 QY 61 QVFWKRAEKQDP 72
 Db 90 QIFLKRKQKDP 101
 RESULT 5
 IL8_PIG STANDARD; PRT; 103 AA.
 ID IL8_PIG
 AC P26894; P22951;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Alveolar macrophage
 DE chemotactic factor 1) (AMCF-1).
 OS Name=IL8;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94103307; PubMed=8276881;
 RA Lin G., Pearson A.B., Scamurra R.W., Zhou Y., Baarsch M.J.,
 RA Weiss D.J., Murttaugh M.P.;
 RT "Regulation of interleukin-8 expression in porcine alveolar
 RT macrophages by bacterial lipopolysaccharide.";
 RL J. Biol. Chem. 269:77-85(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sanjanwala M.;
 RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-45.
 RX MEDLINE=93041741; PubMed=1420165;
 RA Goodman R.B., Foster D.C., Mathews S.L., Osborn S.G., Kufper J.L.,
 RA Forstrom J.W., Martin T.R.;
 RT "Molecular cloning of porcine alveolar macrophage-derived neutrophil
 RT chemotactic factors I and II; identification of porcine IL-8 and
 RT another interleukine-alpha protein.";
 RL Biochemistry 31:10483-10490(1992).
 RN [4]
 RP REVISION TO 23.
 RA Goodman R.B.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 26-45.
 RC STRAIN=Yorkshire;
 RX MEDLINE=91217086; PubMed=1850745;

RA Goodman R.B., Forstrom J.W., Osborn S.G., Chi E.Y., Martin T.R.;
 RT "Identification of two neutrophil chemotactic peptides produced by
 RT porcine alveolar macrophages.";
 RL J. Biol. Chem. 266:8455-8463(1991).
 CC -1- FUNCTION: IL-8 is a chemotactic factor that attracts neutrophils,
 CC basophils, and T-cells, but not monocytes. It is also involved in
 CC neutrophil activation. It is released from several cell types in
 CC response to an inflammatory stimulus.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Alveolar macrophages.
 CC -1- INDUCTION: By lipopolysaccharide (LPS).
 CC -1- SIMILARITY: Belongs to the interleukin alpha (chemokine CXC)
 CC family.
 CC -----
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DR EMBL; M86923; AAA1616.1; -;
 DR EMBL; X61151; CAA4361.1; -;
 DR EMBL; M9367; AAA92576.1; -;
 DR PIR; A39819; A39819.
 DR PIR; A53096; A53096.
 DR HSSP; P10145; 11RM.
 DR InterPro; IPR002473; C-X-C/Interkn_8.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR InterPro; IPR001089; CXC_chemkine_small.
 DR Pfam; PF00048; IL8; 1.
 DR PRINTS; PR00436; INTERLEUKIN8.
 DR PRINTS; SM00437; SMALLCYTCCX.
 DR SMART; SM00199; SCY_1.
 DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
 DR Chemotaxis; Cytokines; Direct protein sequencing;
 KM Inflammatory response; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 103 Interleukin-8.
 FT DISULFID 34 61 By similarity.
 FT DISULFID 36 77 By similarity.
 FT CONFLICT 33 34 RC -> CR (in Ref. 5).
 FT CONFLICT 87 87 K -> KK (in Ref. 2).
 SQ SEQUENCE 103 AA; 11633 MW; 9FE0E350E1928C64 CRC64;

Query Match 85.7%; Score 335; DB 1; Length 103;
 Best Local Similarity 88.4%; Pred. No. 2.4e-30;
 Matches 61; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 ELRCQCIHTSTPFPKFKELRVIESPPHCENSEIIIVKLTNGNEVCINPKKRWQKVVQ 61
 DB 31 ELRCQCIHTSTPFPKFKELRVIESPPHCENSEIIIVKLTNGNEVCINPKKRWQKVVQ 90
 QY 62 VFWKRAEQ 70
 DB 91 IFKRTKQ 99

RESULT 6
 BAC06611 PRELIMINARY; PRT; 103 AA.
 AC BAC06611
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
 DE Interleukin-8.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Shimanuki S., Kobayashi E., Awata T.;
 RT "Genomic structure of the porcine Interleukin 8 gene and development
 RT of a microsatellite marker within intron 1.";
 RL Anim. Genet. 33:470-471(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93041741; PubMed=1420165;
 RA Goodman R., Foster D., Mathews S., Osborn S., Kuiper J.,
 RA Forstrom J., Martin T.;
 RT "Molecular Cloning of Porcine Alveolar Macrophage-Derived Neutrophil
 RT Chemotactic Factors I and II: Identification of Porcine IL8 and
 RT Another Interleukin-a Protein.";
 RL Biochemistry 31:10483-10490(1992).
 DR EMBL; AB057440; BAC06611.1; -;
 SQ SEQUENCE 103 AA; 11633 MW; 9FE0E350E1928C64 CRC64;

Query Match 85.7%; Score 335; DB 2; Length 103;
 Best Local Similarity 88.4%; Pred. No. 2.4e-30;
 Matches 61; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 ELRCQCIHTSTPFPKFKELRVIESPPHCENSEIIIVKLTNGNEVCINPKKRWQKVVQ 61
 DB 31 ELRCQCIHTSTPFPKFKELRVIESPPHCENSEIIIVKLTNGNEVCINPKKRWQKVVQ 90
 QY 62 VFWKRAEQ 70
 DB 91 IFKRTKQ 99

RESULT 7
 IL8-RABIT STANDARD; PRT; 101 AA.
 ID IL8-RABIT
 AC P19874;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Neutrophil
 DE attractant/activation protein-1) (MMP-1) (Permeability factor 1)
 DE (RPP1).
 DE Name=IL8;
 GN Oryctolagus cuniculus (Rabbit).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buthera; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Spleen;
 RX MEDLINE=91225489; PubMed=202677;
 RA Yoshimura T., Yuhki N.;
 RA "Neutrophil attractant/activation protein-1 and monocyte
 RT chemottractant protein-1 in rabbit. cDNA cloning and their expression
 RT in spleen cells.";
 RL J. Immunol. 146:3483-3488(1991).
 RN [2]
 RP SEQUENCE OF 23-53.
 RC STRAIN=New Zealand white; TISSUE=Peritoneal cavity;
 RX MEDLINE=91058518; PubMed=2244880;
 RA Beaudien B.C., Collins P.D., Jose P.J., Totty N.F., Hsuan J.,
 RA Waterfield W.D., Williams T.J.;
 RA "A novel neutrophil chemottractant generated during an inflammatory
 RT reaction in the rabbit peritoneal cavity in vivo. Purification,
 RT partial amino acid sequence and structural relationship to interleukin
 RT 8.";
 RL Blochem. J. 271:797-801(1990).
 CC -1- FUNCTION: IL-8 is a chemotactic factor that attracts neutrophils,
 CC basophils, and T-cells, but not monocytes. It is also involved in
 CC neutrophil activation. It is released from several cell types in
 CC response to an inflammatory stimulus.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the interleukin alpha (chemokine CXC)
 CC family.

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CC -----
CC EMBL; M57439; AAA31422.1; -.
CC PIR; I46871; I46871.
CC HSSP; P10145; 21L8.
CC InterPro; IPR002473; C-X-C/Interlkn_8.
CC InterPro; IPR001811; Chemokine_IL8.
CC InterPro; IPR001089; CXCL_Chemkine_sm11.
CC Pfam; PF00048; IL8; 1.
CC PRINTS; PR00436; INTERLEUKIN8.
CC PRINTS; PR00437; SMALLCYTCKXC.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
CC Chemotaxis; Cytokine; Direct protein sequencing;
CC Inflammatory response; Signal.
CC SIGNAL
FT CHAIN 1 22 Interleukin-8.
FT DISUPID 23 101 By similarity.
FT DISUPID 34 61 By similarity.
FT DISUPID 36 77 By similarity.
FT CONFLICT 50 50 K->I (in Ref. 2).
SQ SEQUENCE 101 AA; 11402 MW; 152B10C43AD8726 CRC64;

Query Match 84.4%; Score 330; DB 1; Length 101;
Best Local Similarity 83.1%; Pred. No. 8.9e-30;
Matches 59; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 TELRCQICIRHSTPFPHKFIKELRVISPPHCENSEIIVLTNGNEVCNPKKWKQKV 60
DB 30 TELRCQICIRHSTPFPHKFIKELRVISPPHCENSEIIVLTNGNEVCNPKKWKQKV 89
QY 61 QVFWKRAEKOD 71
DB 90 QVFWKRAEKOD 100

RESULT 8
IL8_FELCA STANDARD; PRT; 101 AA.
AC G9XSX5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN Name=IL8;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Strabinger A.F., Simpson K.W., Straubinger R.K.;
RT "Feline interleukin-8 mRNA."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL-8 is a chemotactic factor that attracts neutrophils,
CC basophils, and T-cells, but not monocytes. It is also involved in
CC neutrophil activation. It is released from several cell types in
CC response to an inflammatory stimulus (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the Interleukin alpha (chemokine Cx)
CC family.
CC -----
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CC -----
CC EMBL; AF158598; AAD40323.1; -.
CC HSSP; P10145; 1IKM.
CC InterPro; IPR002473; C-X-C/Interlkn_8.
CC InterPro; IPR001811; Chemokine_IL8.
CC InterPro; IPR001089; CXCL_Chemkine_sm11.
CC Pfam; PF00048; IL8; 1.
CC PRINTS; PR00436; INTERLEUKIN8.
CC PRINTS; PR00437; SMALLCYTCKXC.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
CC Chemotaxis; Cytokine; Inflammatory response; Signal.
CC SIGNAL
FT CHAIN 1 22 By similarity.
FT DISUPID 23 101 Interleukin-8.
FT DISUPID 34 61 By similarity.
FT DISUPID 36 77 By similarity.
SQ SEQUENCE 101 AA; 11165 MW; 690D97F13BF79170 CRC64;

Query Match 79.8%; Score 312; DB 1; Length 101;
Best Local Similarity 77.5%; Pred. No. 1e-27;
Matches 55; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 TELRCQICIRHSTPFPHKFIKELRVISPPHCENSEIIVLTNGNEVCNPKKWKQKV 60
DB 30 TELRCQICIRHSTPFPHKFIKELRVISPPHCENSEIIVLTNGNEVCNPKKWKQKV 89
QY 61 QVFWKRAEKOD 71
DB 90 EFWKRAEKON 100

RESULT 9
IL8_MACMU STANDARD; PRT; 101 AA.
AC P51495;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN Name=IL8;
OS Macaca mulatta (Rhesus macaque), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544; 9545;
RN [1]
RP SEQUENCE FROM N.A.
RA SPECIES=M. mulatta, and M. nemestrina; TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Wayne A.B., Chikkala N., Anari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
RT J. Immunol. 155:3946-3954 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA SPECIES=M. mulatta; TISSUE=Blood;
RX MEDLINE=95355132; PubMed=7628861;
RA Minnerly J.C., Bagaroff M.P., Deppele C.L., Keller B.T., Rapp S.R.,
RA Wdowski D.B., Fretland D.J., Bolanowski M.A.;
RT "Identification and characterization of rhesus macaque interleukin-
RT 8."
RL Inflammation 19:313-331 (1995).
CC -1- FUNCTION: IL-8 is a chemotactic factor that attracts neutrophils,
CC basophils, and T-cells, but not monocytes. It is also involved in
CC neutrophil activation. It is released from several cell types in
CC response to an inflammatory stimulus (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the Interleukin alpha (chemokine Cx)

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CC family.
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CC -----
DR EMBL: U19849; AAA86711.1; -
DR EMBL: U19851; AAA86713.1; -
DR EMBL: S78555; AAA80141.2; -
DR HSSP: P10145; 2IL8.
DR InterPro: IPR002473; C-X-C/Interlkn_8.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CX_C_chmkine_sm11.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00436; INTERLEUKIN8.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
KW Chemokine; Cytokine; Inflammatory response; Signal.
FT SIGNAL 1 22 By similarity.
FT CHAIN 23 101 Interleukin-8.
FT DISULFID 34 61 By similarity.
FT DISULFID 36 77 By similarity.
SQ SEQUENCE 101 AA; 11320 MW; 42BCF9C97C84B5F9 CRC64;

Query Match
Best Local Similarity 76.5%; Score 299; DB 1; Length 101;
Matches 53; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 2 ELRCQCIKTHSTDPHFKFKELRVISGPHCENSEIIVLTNGNEVCLNPKKRWQKVQ 61
DB 31 ELRCQCIKTHSTDPHFKFKELRVISGPHCANTETIIVLTNGNEVCLNPKKRWQKVQ 90
QY 62 VFVRAEKODP 72
DB 91 KFYKRAEQNP 101

RESULT 10
ID Q866R3 PRELIMINARY; PRT; 101 AA.
AC Q866R3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Interleukin 8.
OS Name=IL8.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OC NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Cappelli K., Verini-Supplizi A., Silvestrelli M.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY184956; AA037764.1; -
DR HSSP: P10145; 2IL8.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0008009; P:chemokine activity; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR002473; C-X-C/Interlkn_8.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CX_C_chmkine_sm11.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00436; INTERLEUKIN8.
DR PRINTS: PR00437; SMALLCYTOKXC.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
SQ SEQUENCE 101 AA; 11080 MW; E3487811854009A CRC64;

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Query Match
Best Local Similarity 75.7%; Score 296; DB 2; Length 101;
Matches 55; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 2 ELRCQCIKTHSTDPHFKFKELRVISGPHCENSEIIVLTNGNEVCLNPKKRWQKVQ 61
DB 31 ELRCQCIKTHSTDPHFKFKELRVISGPHCENSEIIVLTNGNEVCLNPKKRWQKVQ 90
QY 62 VFVRAEKODP 72
DB 91 AFVRAEQNP 101

RESULT 11
ID Q71UR4 PRELIMINARY; PRT; 56 AA.
AC Q71UR4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Interleukin-8 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99122641; PubMed=9922392;
RA Heaton M.P., Laegreid W.W., Beatrice C.W., Smith T.P.L., Kappes S.M.;
RT "Identification and genetic mapping of bovine chemokine genes
RT expressed in epithelial cells.";
RL Mamm. Genome 10:128-133(1999).
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2118989; PubMed=11252171;
RA Heaton M.P., McKown C.G., Grosse W.M., Keen J.E., Fox J.M.,
RA Laegreid W.W.;
RT "Interleukin-8 haplotype structure from nucleotide sequence variation
RT in commercial populations of US cattle.";
RL Mamm. Genome 12:219-226(2001).
DR EMBL: AF061521; AAD02808.1; -
DR InterPro: IPR002473; C-X-C/Interlkn_8.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CX_C_chmkine_sm11.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00436; INTERLEUKIN8.
DR PRINTS: PR00437; SMALLCYTOKXC.
DR SMART: SM00199; SCY; 1.
FT NON TER 1
SQ SEQUENCE 56 AA; 6474 MW; 827ACE2DAAA784E3 CRC64;

Query Match
Best Local Similarity 73.7%; Score 288; DB 2; Length 56;
Matches 55; Conservative 98.2%; Pred. No. 2.9e-25; Indels 1; Gaps 0;

QY 17 PKFKELRVISGPHCENSEIIVLTNGNEVCLNPKKRWQKVQVFVRAEKODP 72
DB 1 PKFKELRVISGPHCENSEIIVLTNGNEVCLNPKKRWQKVQVFVRAEKODP 56

RESULT 12
ID AAD02808 PRELIMINARY; PRT; 56 AA.
AC AAD02808;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Interleukin-8 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

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OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9122841; PubMed=9922392;
 RA Heaton M.P., Laegreid W.W., Beattie C.W., Smith T.P.L., Kappes S.M.;
 RT "Identification and genetic mapping of bovine chemokine genes
 expressed in epithelial cells."
 RL Mamm. Genome 10:128-133(1999).
 RL [2]
 RN SEQUENCE FROM N.A.
 RA Heaton M.P., McKown C.G., Grosse W.M., Keen J.E., Fox J.M.,
 RA Laegreid W.W.;
 RT "Interleukin-8 haplotype structure from nucleotide sequence variation
 in commercial populations of US cattle."
 RL Mamm. Genome 12:219-225(2001).
 DR EMBL; AF061521; AAD02808.1; -.
 FT NON_TER 1
 SQ SEQUENCE 56 AA; 6474 MW; 827ACB2DAAA784E3 CRC64;
 Query Match 73.7%; Score 288; DB 2; Length 56;
 Best Local Similarity 98.2%; Pred. No. 2.9e-25;
 Matches 55; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 17 PKFKELRVIESPPHCENSEIIVKLTNGNEVCINPKKQVQKVVQVVKAEKQDP 72
 DB 1 PKFKELRVIESGPHCENSEIIVKLTNGNEVCINPKKQVQKVVQVVKAEKQDP 56
 ID OCLAB6 PRELIMINARY; PRT; 97 AA.
 AC OCLAB6;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Interleukin 8 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=91374977; PubMed=1895676;
 RA Kuster D.J., Luebers E.L., Nowinski R.J., Konieczkowski M.,
 RA King C.H., Sedor J.R.;
 RT "Cytokine- and LPS-induced synthesis of interleukin-8 from human
 mesangial cells."
 RL Kidney Int. 39:1240-1248(1991).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX King C.H., Gordon G.S., Konieczkowski M., Sedor J.R.;
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA King C.;
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z11686; CA77745.1; -.
 DR InterPro; IPR002473; C-X-C/Interlkn_8.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR InterPro; IPR001089; CXc_chmkine_sm11.
 DR Pfam; PF00048; IL8; 1.
 DR PRINTS; PR00436; INTERLEUKIN8.
 DR PRINTS; PR00437; SMALLCYTOKC.
 DR SMART; SMO0199; SCY; 1.
 DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
 FT NON_TER 1
 SQ SEQUENCE 97 AA; 10897 MW; 09996B89319F4972 CRC64;

Query Match 73.4%; Score 287; DB 2; Length 97;
 Best Local Similarity 76.1%; Pred. No. 6.9e-25;
 Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
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 DB 31 ELRCOCIKTYSKPFHFKFKIKELRVIESGPHCANTETIIVKLSDRERCLDPKENVQKRV 90
 QY 62 VPKYKRAE 68
 DB 91 KFLKRAE 97
 ID CA77745 PRELIMINARY; PRT; 97 AA.
 AC CA77745;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Interleukin 8 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, cortex;
 RA King C.H., Gordon G.S., Konieczkowski M., Sedor J.R.;
 RT "cDNA cloning of human mesangial cell interleukin 8 by polymerase
 chain reaction."
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, cortex;
 RX MEDLINE=91374977; PubMed=1895676;
 RA Kuster D.J., Luebers E.L., Nowinski R.J., Konieczkowski M.,
 RA King C.H., Sedor J.R.;
 RT "Cytokine- and LPS-induced synthesis of interleukin-8 from human
 mesangial cells."
 RL Kidney Int. 39:1240-1248(1991).
 DR EMBL; Z11686; CA77745.1; -.
 FT NON_TER 1
 FT NON_TER 97
 SQ SEQUENCE 97 AA; 10897 MW; 09996B89319F4972 CRC64;
 Query Match 73.4%; Score 287; DB 2; Length 97;
 Best Local Similarity 76.1%; Pred. No. 6.9e-25;
 Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 QY 2 ELRCOCIRHTSTPFPKFKIKELRVIESPPHCENSEIIVKLTNGNEVCINPKKQVQKVVQ 61
 DB 31 ELRCOCIKTYSKPFHFKFKIKELRVIESGPHCANTETIIVKLSDRERCLDPKENVQKRV 90
 QY 62 VPKYKRAE 68
 DB 91 KFLKRAE 97
 ID IL8_HUMAN STANDARD; PRT; 99 AA.
 AC P10145; Q96RG6; Q9C077;
 DT 01-MAY-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil-
 activating factor) (MDCP) (T-cell chemotactic factor) (Neutrophil-
 activating protein 1) (NAP-1) (Protein 3-10C) (Granulocyte chemotactic
 protein 1) (GCP-1) (Monocyte derived neutrophil activating peptide)
 DE (MOPAP) (Emotakin) (Contains: MDCP-a (IL8/NAP1 form I) (GCP/IL-8
 protein IV); IL-8(1-77) (MDCP-b) (IL8/NAP1 form II) (GCP/IL-8 protein
 II) (ala-IL-8(77); IL-8(6-77) (Lymphocyte-derived neutrophil-


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RT thromboglobulin."
RL Eur. J. Biochem. 181:337-344(1989).
RN [17]
RP N-TERMINAL PROCESSING BY THROMBIN, AND FUNCTION.
RX PubMed=2212672;
RA Hebert C.A., Luscinckas F.W., Kiely J.M., Luis E.A., Darbonne W.C.,
RT Bennett G.L., Liu C.C., Obin M.S., Gimbrone M.A. Jr., Baker J.B.,
RL "Endothelial and leukocyte forms of IL-8. Conversion by thrombin and
  interactions with neutrophils."
  J. Immunol. 145:3033-3040(1990).
RN [18]
RP SYNTHESIS OF 28-99.
RX MEDLINE=9175767; PubMed=2007144;
RA Clark-Lewis I., Mose B., Walz A., Baggiolini M., Scott G.J.,
RL Aebersold R.;
RT "Chemical synthesis, purification, and characterization of two
  inflammatory proteins, neutrophil activating peptide 1 (interleukin-8)
  and neutrophil activating peptide."
  Biochemistry 30:3128-3135(1991).
RN [19]
RP N-TERMINAL PROCESSING BY MMP9.
RX PubMed=11023497;
RA Van den Steen P.E., Proost P., Wuyts A., Van Damme J., Opdenakker G.;
RT "Neutrophil gelatinase B potentiates interleukin-8 tenfold by
  aminoterminal processing, whereas it degrades CTAP-III, PF-4, and GRO-
  alpha and leaves RANTES and MCP-2 intact."
  Blood 96:2673-2681(2000).
RN [20]
RP REVIEW.
RX MEDLINE=92347562; PubMed=1639201;
RA Baggiolini M., Clark-Lewis I.;
RT "Interleukin-8, a chemotactic and inflammatory cytokine."
  FEBS Lett. 307:97-101(1992).
RN [21]
RP REVIEW.
RX PubMed=14711052;
RA Struyf S., Proost P., Van Damme J.;
RT "Regulation of the immune response by the interaction of chemokines
  and proteases."
  Adv. Immunol. 81:1-44(2003).
RN [22]
RP STRUCTURE BY NMR OF 28-99.

Query Match 73.4%; Score 287; DB 1; Length 99;
Best Local Similarity 76.1%; Pred. NO. 7e-25;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 2 ELRCQCIKRTSTPFPKFKELRYIESPPHCENSEIIVKLTNGNEVCLNPKKKVQKQVQ 61
   |||||:|:|||||:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 31 ELRCQCIKRTSKPFPKFKELRYIESPPHCANTEIIVKLTSDGRELCLDPKKNVQKQVVE 90
   |||||:|:|||||:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||

QY 62 VFWKRAE 68
   |:||||
Db 91 KFLKRAE 97

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 Job time : 201 secs

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